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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:25:20 ; Search time 32 Seconds
(without alignments)
327.502 Million cell updates/sec

Title: US-09-869-566-5
Perfect score: 1059
Sequence: 1 MSALLILALVGAIVADYKDD.....IEFSFQVCKAKMSPEVSD 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfilest.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895	84.5	218	4	US-09-293-625-2
2	895	84.5	218	4	US-09-398-412B-4
3	863.5	81.5	218	4	US-09-398-412B-2
4	702	66.3	167	3	US-09-128-155-7
5	702	66.3	178	3	US-09-128-155-2
6	695	65.6	136	3	US-09-128-155-11
7	623	58.8	115	3	US-09-128-155-5
8	623	58.8	115	3	US-09-128-155-9
9	623	58.8	115	3	US-09-128-155-13
10	473.5	44.7	185	3	US-09-128-155-18
11	229.5	21.7	169	2	US-08-790-032-2
12	229.5	21.7	169	3	US-09-069-619-2
13	229.5	21.7	169	4	US-09-494-018-2
14	229.5	21.7	169	4	US-09-398-412B-15
15	191.5	18.1	156	4	US-09-398-412B-13
16	174.5	16.5	155	3	US-09-417-455-5
17	174.5	16.5	155	4	US-09-348-942-5
18	174.5	16.5	155	4	US-09-316-081-5
19	174.5	16.5	155	4	US-09-578-458-5
20	174.5	16.5	155	4	US-09-523-964A-5
21	174.5	16.5	155	4	US-09-457-626-5
22	174.5	16.5	155	4	US-09-576-008-5
23	171	16.1	160	4	US-09-398-412B-14
24	167	15.8	178	3	US-09-000-630C-21
25	167	15.8	178	3	US-08-862-730C-21
26	167	15.8	178	3	US-09-417-455-9
27	167	15.8	178	4	US-09-348-942-9

28	167	15.8	178	4	US-09-457-626-9	Sequence 9, Appli
29	167	15.8	178	4	US-09-576-008-9	Sequence 9, Appli
30	165.5	15.6	152	4	US-09-578-458-18	Sequence 18, Appli
31	161	15.2	180	1	US-08-476-860-13	Sequence 13, Appli
32	161	15.2	180	2	US-08-910-733-13	Sequence 13, Appli
33	161	15.2	180	2	US-08-910-884-13	Sequence 13, Appli
34	158.5	15.0	159	1	US-08-459-811-2	Sequence 2, Appli
35	158.5	15.0	159	2	US-08-484-598-2	Sequence 2, Appli
36	158.5	15.0	159	2	US-08-459-092-2	Sequence 2, Appli
37	158.5	15.0	159	2	US-08-459-814-2	Sequence 2, Appli
38	158.5	15.0	159	2	US-08-425-232-2	Sequence 2, Appli
39	158.5	15.0	159	2	US-08-471-227-3	Sequence 3, Appli
40	158.5	15.0	159	2	US-08-479-140-2	Sequence 2, Appli
41	158.5	15.0	159	3	US-08-477-143-2	Sequence 2, Appli
42	158.5	15.0	159	3	US-09-417-455-14	Sequence 14, Appli
43	158.5	15.0	159	4	US-09-348-942-14	Sequence 14, Appli
44	158.5	15.0	159	4	US-09-316-081-9	Sequence 9, Appli
45	158.5	15.0	159	4	US-09-578-458-9	Sequence 9, Appli

ALIGNMENTS

```
RESULT 1
US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293,625
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-625-2

Query Match      84.5%: Score 895; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.4e-97;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      35 PKVNLNPKKFSIHDDHKKVVLDSGNLIVPDKNYIRPEIFALASSLSASAEKSGPI 94
      |||
Db      50 PKVNLNPKKFSIHDDHKKVVLDSGNLIVPDKNYIRPEIFALASSLSASAEKSGPI 109

Cy      95 LLSVSKBFCCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPPIFYRAQVGSNNMLES 154.
      |||
Db      110 LLSVSKBFCCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPPIFYRAQVGSNNMLES 169

Cy      155 AAHGWFFICSCNCEPVGVTDKFENRKHIEFSFQVCKAKMSPEVSD 203
      |||
Db      170 AAHGWFFICSCNCEPVGVTDKFENRKHIEFSFQVCKAKMSPEVSD 218

RESULT 2
US-09-398-412B-4
; Sequence 4, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
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SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-09-398-412B-4

Query Match
Best Local Similarity 100.0%; Pred. No. 9.4e-97; Length 218;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVKNLPPKFSIHDQHKVLYDSGNLIAVPDKNYIRPEIFPALASSLSASAEKGSPT 94
DB 50 PKVKNLPPKFSIHDQHKVLYDSGNLIAVPDKNYIRPEIFPALASSLSASAEKGSPT 109
QY 95 LIGVSKGEFLCYCDKXGSHPSLQTKKELMKLAQKESARRPFIFYRAQVGSNMLES 154
DB 110 LIGVSKGEFLCYCDKXGSHPSLQTKKELMKLAQKESARRPFIFYRAQVGSNMLES 169
QY 155 AAHGWFICTSCNCEPVGVTDFKFNKHIIEFSFQVCKAEMSPSEVSD 203
DB 170 AAHGWFICTSCNCEPVGVTDFKFNKHIIEFSFQVCKAEMSPSEVSD 218

RESULT 3
US-09-398-412B-2
Sequence 2, Application US/09398412B
Patent No. 6680380
GENERAL INFORMATION:
APPLICANT: Tiansu, Jacqueline C.
TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
FILE REFERENCE: DX0904K
CURRENT APPLICATION NUMBER: US/09/398,412B
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: US 60/100948
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-09-398-412B-2

Query Match
Best Local Similarity 81.5%; Score 863.5; DB 4; Length 218;
Matches 172; Conservative 5; Mismatches 11; Indels 15; Gaps 2;

QY 16 DYKDDDDKLA---AANSALCRGP-----KVKNLNPKKFSIHDQHKVLYDSG 60
DB 16 DWEKDEPQCCLEDPAGSPLFEPISLPTMNFVHRSRKYSINPKKFSIHDQHKVLYDSG 75
QY 61 NLIAVPDKNYIRPEIFPALASSLSASAEKGSPTLIGVSKGEFLCYCDKXGSHPSLQ 120
DB 76 NLIAVPDKNYIRPEIFPALASSLSASAEKGSPTLIGVSKGEFLCYCDKXGSHPSLQ 135
QY 121 KKKKMKLAQKESARRPFIFYRAQVGSNMLESAAHPGWFICTSCNCEPVGVTDFKFN 160
DB 136 KKKKMKLAQKESARRPFIFYRAQVGSNMLESAAHPGWFICTSCNCEPVGVTDFKFN 195
QY 181 RKHIEFSFQVCKAEMSPSEVSD 203
DB 196 RKHIEFSFQVCKAEMSPSEVSD 218

RESULT 4
US-09-128-155-7
Sequence 7, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 167
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-7

Query Match
Best Local Similarity 66.3%; Score 702; DB 3; Length 167;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 64 AVPDKNYIRPEIFPALASSLSASAEKGSPTLIGVSKGEFLCYCDKXGSHPSLQTKKE 123
DB 28 SLPTMNFVHTKIFPALASSLSASAEKGSPTLIGVSKGEFLCYCDKXGSHPSLQTKKE 87
QY 124 KLMKLAQKESARRPFIFYRAQVGSNMLESAAHPGWFICTSCNCEPVGVTDFKFNK 183
DB 88 KLMKLAQKESARRPFIFYRAQVGSNMLESAAHPGWFICTSCNCEPVGVTDFKFNK 147
QY 184 IEFSPQVCKAEMSPSEVSD 203
DB 148 IEFSPQVCKAEMSPSEVSD 167

RESULT 5
US-09-128-155-2
Sequence 2, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 178
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-2

Query Match
Best Local Similarity 66.3%; Score 702; DB 3; Length 178;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 64 AVPDKNYIRPEIFPALASSLSASAEKGSPTLIGVSKGEFLCYCDKXGSHPSLQTKKE 123
DB 39 SLPTMNFVHTKIFPALASSLSASAEKGSPTLIGVSKGEFLCYCDKXGSHPSLQTKKE 98
QY 124 KLMKLAQKESARRPFIFYRAQVGSNMLESAAHPGWFICTSCNCEPVGVTDFKFNK 183
DB 99 KLMKLAQKESARRPFIFYRAQVGSNMLESAAHPGWFICTSCNCEPVGVTDFKFNK 158
QY 184 IEFSPQVCKAEMSPSEVSD 203
DB 159 IEFSPQVCKAEMSPSEVSD 178

RESULT 6
US-09-128-155-11
; Sequence 11, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-11

Query Match 65.8%; Score 623; DB 3; Length 136;
Best Local Similarity 96.3%; Pred. No. 1.4e-73;
Matches 130; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 69 NYIRPEIFALASSISASAEKSPILLGVSKGEFCLYCDKDGQSHPSLQKKKXLMKL 128
Db 2 NFVHTKFFALASSISASAEKSPILLGVSKGEFCLYCDKDGQSHPSLQKKKXLMKL 61
Qy 129 AAQESARPRPIFYRAQVGSNMMLSAHPGMFICTSCNCPYGVTDKFNKRKHIEFSF 188
Db 62 AAQESARPRPIFYRAQVGSNMMLSAHPGMFICTSCNCPYGVTDKFNKRKHIEFSF 121
Qy 189 QPVCKAEMSPSEVSVD 203
Db 122 QPVCKAEMSPSEVSVD 136

RESULT 7
US-09-128-155-5
; Sequence 5, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-5

Query Match 58.8%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-65;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 89 EKGSPIILGVSKGEFCLYCDKDGQSHPSLQKKKXLMKLAQKESARPRPIFYRAQVGS 148
Db 1 EKGSPIILGVSKGEFCLYCDKDGQSHPSLQKKKXLMKLAQKESARPRPIFYRAQVGS 60
Qy 149 NMMLSAHPGMFICTSCNCPYGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSVD 203
Db 61 NMMLSAHPGMFICTSCNCPYGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSVD 115

Db 61 NMMLSAHPGMFICTSCNCPYGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSVD 115
RESULT 8
US-09-128-155-9
; Sequence 9, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-9

Query Match 58.8%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-65;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 EKGSPIILGVSKGEFCLYCDKDGQSHPSLQKKKXLMKLAQKESARPRPIFYRAQVGS 148
Db 1 EKGSPIILGVSKGEFCLYCDKDGQSHPSLQKKKXLMKLAQKESARPRPIFYRAQVGS 60
Qy 149 NMMLSAHPGMFICTSCNCPYGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSVD 203
Db 61 NMMLSAHPGMFICTSCNCPYGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSVD 115

RESULT 9
US-09-128-155-13
; Sequence 13, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-13

Query Match 58.8%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-65;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 89 EKGSPIILGVSKGEFCLYCDKDGQSHPSLQKKKXLMKLAQKESARPRPIFYRAQVGS 148
Db 1 EKGSPIILGVSKGEFCLYCDKDGQSHPSLQKKKXLMKLAQKESARPRPIFYRAQVGS 60
Qy 149 NMMLSAHPGMFICTSCNCPYGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSVD 203
Db 61 NMMLSAHPGMFICTSCNCPYGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSVD 115

RESULT 10
US-09-128-155-18
Sequence 18, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 18
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: synthetically generated
LOCATION: (1)...(185)
OTHER INFORMATION: human sequence predicted using an alignment algorithm which
OTHER INFORMATION: predicts presence of alternatively spliced exons for a protein of
OTHER INFORMATION: interest in a stretch of genomic DNA
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(185)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-128-155-18

Query Match 44.7%; Score 473.5; DB 3; Length 185;
Best Local Similarity 91.8%; Pred. No. 2,1e-47;
Matches 90; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 79 LASSLSASAEKSPILGVSKGFCLYCDKDGSHPSIQLKKEKLMKLAQKESARR 138
DB 71 LSLQGSASAEKSPILGVSKGFCLYCDKDGSHPSIQLKKEKLMKLAQKESARR 129

QY 139 FIFRYAQVGSWMNLESAHPGWFICTSCNCEPVGVTDK 176
DB 130 FIFRYAQVGSWMNLESAHPGWFICTSCNCEPVGIXN 167

RESULT 11
US-08-790-032-2
Sequence 2, Application US/08790032
Patent No. 5863769
GENERAL INFORMATION:
APPLICANT: Young, Peter
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
TITLE OF INVENTION: Beta (IL-1RA)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/790,032
FILING DATE: 28-JAN-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: ATG50051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5031
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-790-032-2

Query Match 21.7%; Score 229.5; DB 2; Length 169;
Best Local Similarity 35.0%; Pred. No. 7,5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;

QY 19 DDDDKLAANSALCRGPKVKNINPKKFSIHDDKVLVLDGNTLAVPDKNYIRPEIFPA 78
DB 7 DADGGRAVYQSMCK-----PIGTINDLNQVWTLQGNLVAVPRSDVTPVTAV 58

QY 79 LASSLSASAE-KGSITLLGVSKGFCLYCDKDGSHPSIQLKKEKLMKLAQKESARR 137
DB 59 ITCKYPEALEGGGDIYIGIQNPENCGLCEKVGEG-PTLQKEKINDLVGGQPPV-K 115

QY 138 FIFRYAQVGSWMNLESAHPGWFICTSCNCEPVGVTDK 177
DB 116 PLFIFYRAKTRGTSTLESVAFPDWFIASS-KRQGPILTISE 154

RESULT 12
US-09-069-619-2
Sequence 2, Application US/09069619
Patent No. 6054559
GENERAL INFORMATION:
APPLICANT: Young, Peter and Lisa Marshall
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
TITLE OF INVENTION: Beta (IL-1RA)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,619
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/007,464; and 08/790,032
FILING DATE: filed 14-JAN-1998; and 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William, T.
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50051-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-069-619-2

Query Match 21.7%; Score 229.5; DB 3; Length 169;
Best Local Similarity 35.0%; Pred. No. 7.5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;

Qy 19 DDDDKLAANALCRGPKVKLNLPKFSIHODHKVLVDSGNLIAVPDKKYIRPEIFFA 78
Db 7 DADGGGRAVYQSMCK-----PITGTINDLNQVWTLQGNLVAAPRSDSVTPVTAV 58
Qy 79 LASSLSASAE-KSPPIILGVSKGFCLYCDKQSHPSIQLKKEKLMKLAQKESARR 137
Db 59 ITCKYPPALBGRDPIYLGIQNPENCLYCEKVEQ--PTIQLKEQKIMDIYGPPEV-K 115
Qy 138 PFIFYRAQVGSMMLESAAHPGWFICTSCNCPNPEVGTDK 177
Db 116 PFLFYRAKTGRTSTLESVAFPDMFTASS-KRDQPIILTSE 154

RESULT 13
US-09-494-018-2

; Sequence 2, Application US/09494018
; Patent No. 6399573
; GENERAL INFORMATION:
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST BETA
; FILE REFERENCE: ATG-50051-D1
; CURRENT APPLICATION NUMBER: US/09/494,018
; EARLIER FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 09/069,619
; EARLIER FILING DATE: 1998-04-29
; EARLIER APPLICATION NUMBER: 09/007,464
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 08/790,032
; EARLIER FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 169
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-494-018-2

Query Match 21.7%; Score 229.5; DB 4; Length 169;
Best Local Similarity 35.0%; Pred. No. 7.5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;

Qy 19 DDDDKLAANALCRGPKVKLNLPKFSIHODHKVLVDSGNLIAVPDKKYIRPEIFFA 78
Db 7 DADGGGRAVYQSMCK-----PITGTINDLNQVWTLQGNLVAAPRSDSVTPVTAV 58
Qy 79 LASSLSASAE-KSPPIILGVSKGFCLYCDKQSHPSIQLKKEKLMKLAQKESARR 137
Db 59 ITCKYPPALBGRDPIYLGIQNPENCLYCEKVEQ--PTIQLKEQKIMDIYGPPEV-K 115
Qy 138 PFIFYRAQVGSMMLESAAHPGWFICTSCNCPNPEVGTDK 177
Db 116 PFLFYRAKTGRTSTLESVAFPDMFTASS-KRDQPIILTSE 154

RESULT 14
US-09-398-412B-15
; Sequence 15, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:

; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reager
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-398-412B-15

Query Match 21.7%; Score 229.5; DB 4; Length 169;
Best Local Similarity 35.0%; Pred. No. 7.5e-19;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;

Qy 19 DDDDKLAANALCRGPKVKLNLPKFSIHODHKVLVDSGNLIAVPDKKYIRPEIFFA 78
Db 7 DADGGGRAVYQSMCK-----PITGTINDLNQVWTLQGNLVAAPRSDSVTPVTAV 58
Qy 79 LASSLSASAE-KSPPIILGVSKGFCLYCDKQSHPSIQLKKEKLMKLAQKESARR 137
Db 59 ITCKYPPALBGRDPIYLGIQNPENCLYCEKVEQ--PTIQLKEQKIMDIYGPPEV-K 115
Qy 138 PFIFYRAQVGSMMLESAAHPGWFICTSCNCPNPEVGTDK 177
Db 116 PFLFYRAKTGRTSTLESVAFPDMFTASS-KRDQPIILTSE 154

RESULT 15
US-09-398-412B-13
; Sequence 13, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:

; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reager
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-398-412B-13

Query Match 18.1%; Score 191.5; DB 4; Length 156;
Best Local Similarity 35.1%; Pred. No. 1.9e-14;
Matches 53; Conservative 24; Mismatches 51; Indels 23; Gaps 6;

Qy 28 NSALCRGPKVKLNLPKFSIHODHKVLVDSGNLIA--VPDKKYIRPEIFALASSLS 85
Db 5 SGNLC-----FRKDSALKVLVHNNQLAAGLHAKEVINGEISVPRNALD 52
Qy 86 ASAEKSPPIILGVSKGFCLYCDKQSHPSIQLKKEKLMKLAQKESARRPFIYRA 144
Db 53 ASL---SPVILGVQSGQCLSCGTEKG---PIKLEPVNIMELYLAKES--KSFTFYRR 104
Qy 145 QVGSMMLESAAHPGWFICTSCNCPNPEVGT 175
Db 105 DWGLTSSFEESAAYPGWFLCTSPADQPVRLT 135

Search completed: September 9, 2004, 13:29:59
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:23:09 ; Search time 48 Seconds

(without alignments)
1356.250 Million cell updates/sec

Title: US-09-869-566-5

Perfect score: 1059

Sequence: 1 MSALLILALVNAAYADYKD.....IEFSFQVCKAEKMPSEUSD 203

Scoring table:

BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications AA:
2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	906	85.6	192	10 US-09-876-790-3	Sequence 3, Appl1
2	906	85.6	192	14 US-10-139-833-13	Sequence 13, Appl1
3	902	85.2	197	10 US-09-876-790-9	Sequence 9, Appl1
4	895	84.5	198	9 US-09-788-963-6	Sequence 6, Appl1
5	895	84.5	218	9 US-09-788-963-2	Sequence 2, Appl1
6	895	84.5	218	10 US-09-876-790-8	Sequence 8, Appl1
7	895	84.5	218	12 US-10-695-195-4	Sequence 4, Appl1
8	895	84.5	218	14 US-10-139-833-12	Sequence 12, Appl1
9	895	84.5	218	14 US-10-302-554-2	Sequence 2, Appl1
10	895	84.5	218	16 US-10-684-978-4	Sequence 4, Appl1
11	895	84.5	218	16 US-10-679-201-6	Sequence 4, Appl1
12	891	84.1	218	14 US-10-302-554-14	Sequence 14, Appl1
13	885	83.6	193	12 US-10-063-745-142	Sequence 142, App
14	885	83.6	193	12 US-10-063-512-142	Sequence 142, App
15	885	83.6	193	12 US-10-063-513-142	Sequence 142, App

16	885	83.6	193	12 US-10-063-515-142	Sequence 142, App
17	885	83.6	193	12 US-10-063-549-142	Sequence 142, App
18	885	83.6	193	12 US-10-063-569-142	Sequence 142, App
19	885	83.6	193	12 US-10-063-551-142	Sequence 142, App
20	885	83.6	193	12 US-10-063-555-142	Sequence 142, App
21	885	83.6	193	12 US-10-063-563-142	Sequence 142, App
22	885	83.6	193	12 US-10-063-594-142	Sequence 142, App
23	885	83.6	193	12 US-10-063-553-142	Sequence 142, App
24	885	83.6	193	12 US-10-063-554-142	Sequence 142, App
25	885	83.6	193	13 US-10-066-867-142	Sequence 142, App
26	885	83.6	193	13 US-10-063-547-142	Sequence 142, App
27	885	83.6	193	14 US-10-063-516-142	Sequence 142, App
28	885	83.6	193	14 US-10-063-502-142	Sequence 142, App
29	885	83.6	193	14 US-10-063-518-142	Sequence 142, App
30	885	83.6	193	14 US-10-063-598-142	Sequence 142, App
31	885	83.6	193	14 US-10-227-693-142	Sequence 142, App
32	885	83.6	193	14 US-10-063-567-142	Sequence 142, App
33	885	83.6	193	14 US-10-063-538-142	Sequence 142, App
34	885	83.6	193	14 US-10-063-599-142	Sequence 142, App
35	885	83.6	193	14 US-10-063-595-142	Sequence 142, App
36	885	83.6	193	14 US-10-063-580-142	Sequence 142, App
37	885	83.6	193	14 US-10-063-557-142	Sequence 142, App
38	885	83.6	193	14 US-10-063-585-142	Sequence 142, App
39	885	83.6	193	14 US-10-063-588-142	Sequence 142, App
40	885	83.6	193	14 US-10-063-735-142	Sequence 142, App
41	885	83.6	193	14 US-10-063-526-142	Sequence 142, App
42	885	83.6	193	14 US-10-063-586-142	Sequence 142, App
43	885	83.6	193	14 US-10-063-546-142	Sequence 142, App
44	885	83.6	193	14 US-10-063-564-142	Sequence 142, App
45	885	83.6	193	14 US-10-063-662-142	Sequence 142, App

ALIGNMENTS

RESULT 1
US-09-876-790-3
Sequence 3, Application US/09876790
Publication No. US2003091532A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECE DNAS AND POLYPEPTI
FILE REFERENCE: 2008-US
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-790-3

Query Match 85.6%; Score 906; DB 10; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.7e-91;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 33 RGPVKNLNPKEFIRHDDHVLVDSCNLIAPVDKVIPEIPFALASSISAAKGS 92
DB 22 RGPVKNLNPKEFIRHDDHVLVDSCNLIAPVDKVIPEIPFALASSISAAKGS 81
OY 93 PILVSGKEFCVLCDDKQSGHPSLQKKKELMKLAQKESARPFIFRAQGVNMML 152
DB 82 PILVSGKEFCVLCDDKQSGHPSLQKKKELMKLAQKESARPFIFRAQGVNMML 141

QY 153 ESAAHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 203
DB 142 ESAAHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 192

RESULT 2

US-10-139-833-13
Sequence 13, Application US/10139833
Publication No. US20030004106A1
GENERAL INFORMATION:
APPLICANT: Satis, Christiaan M.
APPLICANT: Giles, Jennifer
APPLICANT: Mu, Sharon X.
APPLICANT: Xia, Min
APPLICANT: Baes, Michael B.
APPLICANT: Craveiro, Roger
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
FILE REFERENCE: 00-1213-E
CURRENT APPLICATION NUMBER: US/10/139, 833
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/170,191
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/188,053
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/194,521
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: 60/195,910
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 09/724,583
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 13
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-10-139-833-13

Query Match 85.6%; Score 906; DB 14; Length 192;
Best Local Similarity 100.0%; Pred. No. 4,7e-91;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 RGRKVNLPKPKFSIHDDHKLVLVDSGNLAVDPKNYIRPEIFPALASSLSASAEKGS 92
DB 22 RGRKVNLPKPKFSIHDDHKLVLVDSGNLAVDPKNYIRPEIFPALASSLSASAEKGS 81
QY 93 PILGVSKGFCLYCDKXGSHPSLOLKKELMKLAQKESARRPFIYRAQVGSNNML 152
DB 82 PILGVSKGFCLYCDKXGSHPSLOLKKELMKLAQKESARRPFIYRAQVGSNNML 141
QY 153 ESAAHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 203
DB 142 ESAAHPGMFICTSCNCPGVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 192

RESULT 3

US-09-876-790-9
Sequence 9, Application US/09876790
Publication No. US20030091532A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECE2 DNAS AND POLYPEPT
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/09/876,790
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549

PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In version 3.1
SEQ ID NO 9
LENGTH: 197
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-790-9

Query Match 85.2%; Score 902; DB 10; Length 197;
Best Local Similarity 91.5%; Pred. No. 1.4e-90;
Matches 172; Conservative 4; Mismatches 6; Indels 6; Gaps 1;

QY 16 DYKDDDKLAANSAALCRGPKVKNLNPKKFSIHDDHKLVLVDSGNLAVDPKNYIRPEI 75
DB 16 DWEKDEPQ-----CLEGPKVKNLNPKKFSIHDDHKLVLVDSGNLAVDPKNYIRPEI 69
QY 76 FFLASSLSASAEKGSPIILGVSKGFCLYCDKXGSHPSLOLKKELMKLAQKESA 135
DB 70 FFLASSLSASAEKGSPIILGVSKGFCLYCDKXGSHPSLOLKKELMKLAQKESA 129
QY 136 RRPFIYRAQVGSNNMLSAHPGWFICTSCNCPGVGVTDKFENRKHIEFSFQPVCKAE 195
DB 130 RRPFIYRAQVGSNNMLSAHPGWFICTSCNCPGVGVTDKFENRKHIEFSFQPVCKAB 189
QY 196 MSPSEVSD 203
DB 190 MSPSEVSD 197

RESULT 4

US-09-788-963-6
Sequence 6, Application US/09788963
Patent No. US20020052473A1
GENERAL INFORMATION:
APPLICANT: YOUNG, PETER R.
APPLICANT: MCDONNELL, PETER C.
APPLICANT: KUMAR, SANJAY
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
FILE REFERENCE: GP-70607-1C1
CURRENT APPLICATION NUMBER: US/09/788,963
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/293,625
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 09/452,140
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 198
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-788-963-6

Query Match 84.5%; Score 895; DB 9; Length 198;
Best Local Similarity 100.0%; Pred. No. 8e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKYKNLNPKKFSIHDDHKLVLVDSGNLAVDPKNYIRPEIFPALASSLSASAEKGSPI 94
DB 30 PKYKNLNPKKFSIHDDHKLVLVDSGNLAVDPKNYIRPEIFPALASSLSASAEKGSPI 89
QY 95 ILGVSKGFCLYCDKXGSHPSLOLKKELMKLAQKESARRPFIYRAQVGSNNMLBS 154
DB 90 ILGVSKGFCLYCDKXGSHPSLOLKKELMKLAQKESARRPFIYRAQVGSNNMLBS 149
QY 155 AAHPGWFICTSCNCPGVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 203
DB 150 AAHPGWFICTSCNCPGVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 198

RESULT 5

US-09-788-963-2

Sequence 2, Application US/09788963
Patent No. US20020052473A1
GENERAL INFORMATION:
APPLICANT: YOUNG, PETER R.
APPLICANT: MCDONNELL, PETER C.
APPLICANT: KUMAR, SANJAY
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
FILE REFERENCE: GP-70607-1C1
CURRENT APPLICATION NUMBER: US/09/788,963
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/293,625
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 09/452,140
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 218
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-788-963-2

Query Match 84.5%; Score 895; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVNLNPKKFSIHQDHKVLVLDGSLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 94
DB 50 PKVNLNPKKFSIHQDHKVLVLDGSLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 109
QY 95 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 154
DB 110 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 169
QY 155 AAHPGFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 203
DB 170 AAHPGFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218

RESULT 6
US-09-876-790-8
Sequence 8, Application US/09876790
Publication No. US20030091532A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECE DNAS AND POLYPEPTI
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/09/876,790
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent version 3.1
SEQ ID NO 8
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-790-8

Query Match 84.5%; Score 895; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVNLNPKKFSIHQDHKVLVLDGSLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 94
DB 50 PKVNLNPKKFSIHQDHKVLVLDGSLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 109

QY 95 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 154
DB 110 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 169
QY 155 AAHPGFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 203
DB 170 AAHPGFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218

RESULT 7
US-10-695-195-4
Sequence 4, Application US/10695195
Publication No. US20040068099A1
GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-695-195-4

Query Match 84.5%; Score 895; DB 12; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.1e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVNLNPKKFSIHQDHKVLVLDGSLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 94
DB 50 PKVNLNPKKFSIHQDHKVLVLDGSLIAPVDKNYIRPEIFPALASSLSASAEKSGSPI 109
QY 95 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 154
DB 110 LIGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPFIYRAOVGSNNMLES 169
QY 155 AAHPGFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 203
DB 170 AAHPGFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218

RESULT 8
US-10-139-833-12
Sequence 12, Application US/10139833
Publication No. US20030094106A1

GENERAL INFORMATION:
APPLICANT: Saris, Christiaan M.
APPLICANT: Giles, Jennifer
APPLICANT: Wu, Sharon X.
APPLICANT: Xia, Min
APPLICANT: Bass, Michael B.
APPLICANT: Cravetto, Roger
TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
FILE REFERENCE: 00-1213-E
CURRENT APPLICATION NUMBER: US/10/139,833
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/170,191
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/188,053
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/194,521
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: 60/195,910
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 09/724,583
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-10-139-833-12

Query Match 84.5%; Score 895; DB 14; Length 218;
Best Local Similarity 100.0%; Pred. No. 9,1e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKYKLNPPKFSIHDDHKLVLVDSGNLAVDPKNTIREIFPALLASSLSASAEGSP1 94
DB 50 PKYKLNPPKFSIHDDHKLVLVDSGNLAVDPKNTIREIFPALLASSLSASAEGSP1 109
QY 95 LIGVSKGEFLCYCDKXGSHPSLQKKKMLKLAQKESARRPFIYRAQVGSNMLES 154
DB 110 LIGVSKGEFLCYCDKXGSHPSLQKKKMLKLAQKESARRPFIYRAQVGSNMLES 169
QY 155 AAHPGWFICTSCNCPNPGVTDKFEENRKHIEFSFQVCAEMSPSEVSD 203
DB 170 AAHPGWFICTSCNCPNPGVTDKFEENRKHIEFSFQVCAEMSPSEVSD 218

RESULT 9
US-10-302-554-2
Sequence 2, Application US/10302554
Publication No. US20030148467A1
GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4
FILE REFERENCE: 98-59
CURRENT APPLICATION NUMBER: US/10/302,554
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/428,118
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 60/105,824
PRIOR FILING DATE: 1998-10-27
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
US-10-302-554-2

Query Match 84.5%; Score 895; DB 14; Length 218;
Best Local Similarity 100.0%; Pred. No. 9,1e-90;

Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 PKYKLNPPKFSIHDDHKLVLVDSGNLAVDPKNTIREIFPALLASSLSASAEGSP1 94
DB 50 PKYKLNPPKFSIHDDHKLVLVDSGNLAVDPKNTIREIFPALLASSLSASAEGSP1 109
QY 95 LIGVSKGEFLCYCDKXGSHPSLQKKKMLKLAQKESARRPFIYRAQVGSNMLES 154
DB 110 LIGVSKGEFLCYCDKXGSHPSLQKKKMLKLAQKESARRPFIYRAQVGSNMLES 169
QY 155 AAHPGWFICTSCNCPNPGVTDKFEENRKHIEFSFQVCAEMSPSEVSD 203
DB 170 AAHPGWFICTSCNCPNPGVTDKFEENRKHIEFSFQVCAEMSPSEVSD 218

RESULT 10
US-10-694-978-4
Sequence 4, Application US/10694978
Publication No. US20040087766A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/694,978
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-694-978-4

Query Match 84.5%; Score 895; DB 16; Length 218;
Best Local Similarity 100.0%; Pred. No. 9,1e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKYKLNPPKFSIHDDHKLVLVDSGNLAVDPKNTIREIFPALLASSLSASAEGSP1 94
DB 50 PKYKLNPPKFSIHDDHKLVLVDSGNLAVDPKNTIREIFPALLASSLSASAEGSP1 109
QY 95 LIGVSKGEFLCYCDKXGSHPSLQKKKMLKLAQKESARRPFIYRAQVGSNMLES 154
DB 110 LIGVSKGEFLCYCDKXGSHPSLQKKKMLKLAQKESARRPFIYRAQVGSNMLES 169
QY 155 AAHPGWFICTSCNCPNPGVTDKFEENRKHIEFSFQVCAEMSPSEVSD 203
DB 170 AAHPGWFICTSCNCPNPGVTDKFEENRKHIEFSFQVCAEMSPSEVSD 218

RESULT 11

US-10-679-201-6
; Sequence 6, Application US/10679201
; Publication No. US20040120923a1
; GENERAL INFORMATION:
; APPLICANT: DINARELLO, CHARLES A.
; APPLICANT: KIM, SOO-HYUN
; APPLICANT: BUTLER, PHILIP
; TITLE OF INVENTION: METHOD OF TREATMENT USING A CYTOKINE ABLE TO BIND
; TITLE OF INVENTION: IL-18BP TO INHIBIT THE ACTIVITY OF A SECOND CYTOKINE
; FILE REFERENCE: 057878-000011
; CURRENT APPLICATION NUMBER: US/10/679,201
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/416,827
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-679-201-6

Query Match 84.5%; Score 895; DB 16; Length 218;

Best Local Similarity 100.0%; Pred. No. 9.1e-90; Indels 0; Gaps 0;
Matches 169; Conservative 0; Mismatches 0;

QY 35 PKVNLNPKKFSIHQDHKVLVLDGNIIVADKNYIRPEIFALASSLSASAEGSPITL 94

DB 50 PKVNLNPKKFSIHQDHKVLVLDGNIIVADKNYIRPEIFALASSLSASAEGSPITL 109

QY 95 LIGVSKGEFCLYCDKDGQSHPSLQTKKELMKLAQKESARRPFIYRAQVGSNNMLES 154

DB 110 LIGVSKGEFCLYCDKDGQSHPSLQTKKELMKLAQKESARRPFIYRAQVGSNNMLES 169

QY 155 AAHGMFICTSCNCPNPGVTDKFNKRKHIEFSFPVCKAEMSPSEVSD 203

DB 170 AAHGMFICTSCNCPNPGVTDKFNKRKHIEFSFPVCKAEMSPSEVSD 218

RESULT 12

US-10-302-554-14
; Sequence 14, Application US/10302554
; Publication No. US20030148467a1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4
; FILE REFERENCE: 98-59
; CURRENT APPLICATION NUMBER: US/10/302,554
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US/09/428,118
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 60/105,824
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant protein
US-10-302-554-14

Query Match 84.1%; Score 891; DB 14; Length 218;
Best Local Similarity 99.4%; Pred. No. 2.5e-89;
Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVNLNPKKFSIHQDHKVLVLDGNIIVADKNYIRPEIFALASSLSASAEGSPITL 94

DB 50 PKVNLNPKKFSIHQDHKVLVLDGNIIVADKNYIRPEIFALASSLSASAEGSPITL 109

QY 95 LIGVSKGEFCLYCDKDGQSHPSLQTKKELMKLAQKESARRPFIYRAQVGSNNMLES 154

DB 110 LIGVSKGEFCLYCDKDGQSHPSLQTKKELMKLAQKESARRPFIYRAQVGSNNMLES 169

QY 155 AAHGMFICTSCNCPNPGVTDKFNKRKHIEFSFPVCKAEMSPSEVSD 203

DB 170 AAHGMFICTSCNCPNPGVTDKFNKRKHIEFSFPVCKAEMSPSEVSD 218

RESULT 13

US-10-063-745-142
; Sequence 142, Application US/10063745
; Publication No. US20040058411a1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 142
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-745-142

Query Match 83.6%; Score 885; DB 12; Length 193;
Best Local Similarity 99.4%; Pred. No. 9.7e-89;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 KVNKLNPKKFSIHQDHKVLVLDGNIIVADKNYIRPEIFALASSLSASAEGSPITL 95

DB 26 KVNKLNPKKFSIHQDHKVLVLDGNIIVADKNYIRPEIFALASSLSASAEGSPITL 85

QY 96 LIGVSKGEFCLYCDKDGQSHPSLQTKKELMKLAQKESARRPFIYRAQVGSNNMLES 155

DB 86 LIGVSKGEFCLYCDKDGQSHPSLQTKKELMKLAQKESARRPFIYRAQVGSNNMLES 145

QY 156 AHPGMFICTSCNCPNPGVTDKFNKRKHIEFSFPVCKAEMSPSEVSD 203

DB 146 AHPGMFICTSCNCPNPGVTDKFNKRKHIEFSFPVCKAEMSPSEVSD 193

RESULT 14

US-10-063-512-142
; Sequence 142, Application US/10063512
; Publication No. US20030018183a1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1

; CURRENT APPLICATION NUMBER: US/10/063,512
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 142
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-063-512-142

Query Match 83.6%; Score 885; DB 12; Length 193;
 Best Local Similarity 99.4%; Pred. No. 9,7e-89;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 KVNKNLPKFKSIHQDQHKVILVDSGNLIAPDKNYIRPEIFPALASSLSASAEKGSPTL 95
 :
 Db 26 RVKNLNPKFKSIHQDQHKVILVDSGNLIAPDKNYIRPEIFPALASSLSASAEKGSPTL 85
 QY 96 LGVSKGEFCLCYCDKQSHPSLQKKKKLMLAOKESARPPFIFFRAQVGSNMMLESA 155
 :
 Db 86 LGVSKGEFCLCYCDKQSHPSLQKKKKLMLAOKESARPPFIFFRAQVGSNMMLESA 145
 QY 156 AHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 203
 :
 Db 146 AHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 193

RESULT 15

US-10-063-513-142
 ; Sequence 142, Application US/10063513
 ; Publication No. US20030018172A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P9230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,513
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 142
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-063-513-142

Query Match 83.6%; Score 885; DB 12; Length 193;
 Best Local Similarity 99.4%; Pred. No. 9,7e-89;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 KVNKNLPKFKSIHQDQHKVILVDSGNLIAPDKNYIRPEIFPALASSLSASAEKGSPTL 95
 :
 Db 26 RVKNLNPKFKSIHQDQHKVILVDSGNLIAPDKNYIRPEIFPALASSLSASAEKGSPTL 85
 QY 96 LGVSKGEFCLCYCDKQSHPSLQKKKKLMLAOKESARPPFIFFRAQVGSNMMLESA 155
 :
 Db 86 LGVSKGEFCLCYCDKQSHPSLQKKKKLMLAOKESARPPFIFFRAQVGSNMMLESA 145
 QY 156 AHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 203
 :
 Db 146 AHPGWFICTSCNCPNPEVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 193

Search completed: September 9, 2004, 13:29:22
 Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:11:59 / Search time 123 Seconds
(without alignments)
466.318 Million cell updates/sec

Title: US-09-869-566-5
Perfect score: 1059
Sequence: 1 MSALLILATVGAADVADYKDD.....IEFSFQPVCKAEMSPSEVSD 203

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1059	100.0	203	3	AAV96933 Human IL-
2	906	85.6	192	3	AAV95297 Human int
3	902	85.2	197	3	AAV95300 Human int
4	895	84.5	198	4	AAV95138 Interleuk
5	895	84.5	207	3	AAV96938 Human IL-
6	895	84.5	218	3	AAV70927 Human IL-
7	895	84.5	218	3	AAV91885 Primate i
8	895	84.5	218	3	AAV95299 Human int
9	895	84.5	218	3	AAV96940 Human IL-
10	895	84.5	218	3	AAV96934 Human int
11	895	84.5	218	4	AAV847186 IL-1 re
12	895	84.5	218	4	AAV68116 Human int
13	895	84.5	218	4	AAV85136 Interleuk
14	892	84.2	218	3	AAV71084 Human zil
15	891	84.1	218	3	AAV70933 Human zil
16	885	83.6	193	3	AAV96934 Proc
17	885	83.6	193	4	AAV87596 Human PRO
18	885	83.6	193	5	ABG95921 Human sec
19	885	83.6	193	6	ABU90946 Novel hum
20	885	83.6	193	6	ABO34005 Human sec
21	885	83.6	193	6	ABU72022 Novel hum
22	885	83.6	193	6	ABU71576 Human sec
23	885	83.6	193	6	ABU91030 Human PRO
24	885	83.6	193	6	ABO27351 Human sec
25	885	83.6	193	6	ABU92546 Human sec

26	885	83.6	193	6	ABU81216 Human sec
27	885	83.6	193	6	ABO53330 Novel hum
28	885	83.6	193	6	ABU98333 Novel hum
29	885	83.6	193	6	ABU89338 Novel hum
30	885	83.6	193	6	ABU82545 Novel hum
31	885	83.6	193	6	ABU96509 Human PRO
32	885	83.6	193	6	ABU72179 Human PRO
33	885	83.6	193	6	ADBI17199 Human tra
34	885	83.6	193	6	ABO44309 Human sec
35	885	83.6	193	6	ADA20004 Novel hum
36	885	83.6	193	6	ADBI17387 Human tra
37	885	83.6	193	6	ADA20176 Novel hum
38	885	83.6	193	6	ABO34237 Human sec
39	885	83.6	193	6	ADA00473 Human sec
40	885	83.6	193	7	ADB85715 Novel hum
41	885	83.6	193	7	ADB68394 Human PRO
42	885	83.6	193	7	ADB68201 Human PRO
43	885	83.6	193	7	ADB91018 Novel hum
44	885	83.6	193	7	ADC07098 Human PRO
45	885	83.6	193	7	ADC17277 Mammalian

ALIGNMENTS

RESULT 1
ID AAV96933 standard; protein: 203 AA.
XX
AC AAV96933;
DT 31-OCT-2000 (first entry)
XX
DE Human IL-1RA fused to heterologous signal sequence.
XX
KW hIL-1RA; human interleukin-1 receptor antagonist-1; IL-1p; osteopathic;
KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;
KW dermatological; immunomodulatory; gastrointestinal; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..15
FT Peptide /label= Signal_peptide
FT Peptide 16..23
FT Peptide /label= Flag_tag
FT Peptide 24..36
FT Peptide /label= linker
FT Protein 37..203
FT /label= hIL-1RA1
XX
MO200039297-A2.
PD 06-JUL-2000.
XX
PE 22-DEC-1999; 99WO-US030720.
XX
PR 23-DEC-1998; 98US-0113430P.
PR 22-JAN-1999; 99US-0116843P.
PR 13-APR-1999; 99US-0129122P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Pan J; Audrey
XX WPI; 2000-452395/39.
XX N-PSDB; AA51592.
XX Nucleic acid encoding interleukin-1-like polypeptides, useful for
XX preventing and treating e.g. inflammation, asthma and psoriasis.
XX Claim 22; Fig 2; 143pp; English.
PS

XX An isolated nucleic acid molecule encoding an interleukin-1-like
 CC polypeptide (IL-11p) that retains one or more activities of the peptide
 CC from which it is derived, such as the IL-18R binding activity of a human
 CC interleukin-1 receptor antagonist-1 (IL-1Ra1) polypeptide, is new. The
 CC nucleic acids may be used in molecular engineering applications, e.g.
 CC hybridization assays and chromosome and gene mapping studies, for
 CC recombinantly producing the IL-11p polypeptide or for producing gene
 CC knock out animals to study the role of the protein in metabolism and
 CC disease processes (conversely, gene therapy protocols may be used to
 CC supplement a patient's production of the polypeptide or to rectify
 CC mutations that lead to the production of an active peptide). The
 CC peptides produced may be used to screen for and produce modulators (e.g.
 CC antibodies) of IL-11p protein expression and activity which may be used to
 CC treat disorders associated with inappropriate IL-11p expression and
 CC activity, such as inflammatory disorders, asthma, arthritis,
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease

XX Sequence 203 AA:

Query Match 100.0%; Score 1059; DB 3; Length 203;
 Best Local Similarity 100.0%; Pred. No. 2e-113;
 Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSALLILALVGAADVADYKDDDDKLAANSAALCGPKVKNLNPKKFSIHDDHKVYLVDG 60
 Db 1 MSALLILALVGAADVADYKDDDDKLAANSAALCGPKVKNLNPKKFSIHDDHKVYLVDG 60
 QY 61 NLIAVDDKNYIRPEIFFALASSLSASAEKGSPIILGVSKGEFCLYCDKDGQSHPSLQL 120
 Db 61 NLIAVDDKNYIRPEIFFALASSLSASAEKGSPIILGVSKGEFCLYCDKDGQSHPSLQL 120
 QY 121 KKKKMLKLAQKESARRPFIFYRAQVGSWMLESAAHPGWFICTSCNCEPVGTTDKFEN 180
 Db 121 KKKKMLKLAQKESARRPFIFYRAQVGSWMLESAAHPGWFICTSCNCEPVGTTDKFEN 180
 QY 181 RKHIESFQPCAKEMSPSEVSD 203
 Db 181 RKHIESFQPCAKEMSPSEVSD 203

RESULT 2

AA95297
 ID AAY95297 standard; protein; 192 AA.

AC AAY95297;

DT 12-SEP-2000 (first entry)

DE Human interleukin-1 zeta.

XX Interleukin-1 zeta; IL-1 zeta; human; therapy; inflammation; fever.

OS Homo sapiens.

PN MO200036108-A2.

PD 22-JUN-2000.

PF 14-DEC-1999; 99MO-US029549.

PR 14-DEC-1998; 98US-0112163P.

PR 10-NOV-1999; 99US-0164675P.

PA (IMMV) IMMUNEX CORP.

PI Sims JE, Smith DE, Born TL;

XX WPI; 2000-442387/38.

XX N-PSDB; AAA27918.

PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
 PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
 PT identifying genes associated with diseases such as glaucoma, and insulin-
 PT dependent diabetes mellitus.

PS Claim 10, Page 8; 87pp; English.

XX The present sequence is that of human interleukin-1 zeta (IL-1 zeta), a
 CC member of the IL-1 family. The sequence was determined by translation of
 CC the nucleotide sequence of isolated IL-1 zeta cDNA (see AAA27918). IL-1
 CC zeta mRNA is generated from exons 3-6 of the IL-1 zeta locus. The mRNA is
 CC expressed most strongly in the testis, prostate, colon, brain, placenta,
 CC lung, foetal liver and lymph node stroma, lung, testis and placenta. The
 CC invention is directed to novel, purified and isolated IL-1 zeta, IL-1
 CC zeta splice variants and Xrec2 polypeptides (see AAY95297-301), the
 CC nucleic acids (see AAA27918-22) encoding such polypeptides, processes for
 CC production of recombinant forms of such polypeptides, and their uses. The
 CC polypeptides can be used to study cellular processes such as immune
 CC regulation, cell proliferation, cell death, cell migration, cell-to-cell
 CC interaction and inflammatory responses, to identify proteins associated
 CC with IL-1 zeta, to screen for potential inhibitors, and to prepare
 CC antibodies. In particular, they can be used to activate and/or inhibit
 CC the activation of vascular endothelial cells and lymphocytes, induce
 CC and/or inhibit the induction of local tissue destruction and fever,
 CC inhibit and/or stimulate macrophages and vascular endothelial cells to
 CC produce IL-6, induce and/or inhibit the induction of prostaglandins,
 CC nitric oxide synthetase, and metalloproteinases, and upregulate and/or
 CC inhibit the upregulation of molecules on the surface of vascular
 CC endothelial cells

XX Sequence 192 AA:

Query Match 85.6%; Score 906; DB 3; Length 192;
 Best Local Similarity 100.0%; Pred. No. 8.4e-96;
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 RGPVKNLNPKKFSIHDDHKVYLVDGSLNLAIPDKNYIRPEIFFALASSLSASAEKGS 92
 Db 22 RGPVKNLNPKKFSIHDDHKVYLVDGSLNLAIPDKNYIRPEIFFALASSLSASAEKGS 81

QY 93 PIIIVSKGEFCLYCDKDGQSHPSIQLKKEKMLKLAQKESARRPFIFYRAQVGSWMNL 152
 Db 82 PIIIVSKGEFCLYCDKDGQSHPSIQLKKEKMLKLAQKESARRPFIFYRAQVGSWMNL 141

QY 153 ESAAHPGWFICTSCNCEPVGTTDKFENRKHIEFSFQPCAKEMSPSEVSD 203
 Db 142 ESAAHPGWFICTSCNCEPVGTTDKFENRKHIEFSFQPCAKEMSPSEVSD 192

RESULT 3

AA95300
 ID AAY95300 standard; protein; 197 AA.

AC AAY95300;

DT 12-SEP-2000 (first entry)

DE Human interleukin-1 zeta splice variant TDZ.2.

XX Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.2;

KW testis-derived zeta variant; therapy; inflammation; fever.

OS Homo sapiens.

PN MO200036108-A2.

PD 22-JUN-2000.

PF 14-DEC-1999; 99MO-US029549.

PR 14-DEC-1998; 98US-0112163P.

PR 10-NOV-1999; 99US-0164675P.

XX

XX

XX

PA (IMMV) IMMUNEX CORP.
 XX
 PI Sime JE, Smith DE, Born TL;
 XX
 DR WPI; 2000-442387/38.
 XX N-PSDB; AAA27921.
 PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
 PT TD21, TD22, TD23 and their encoding proteins, useful as probes for
 PT identifying genes associated with diseases such as glaucoma, and insulin-
 PT dependent diabetes mellitus.
 XX
 PS Claim 10; Page 11; 87pp; English.
 XX
 CC The present sequence is that of splice variant TD2.2 (testis-derived zeta
 CC variant) of human interleukin-1 zeta (IL-1 zeta). TD2.2 mRNA is generated
 CC from exons 1, 4, 5 and 6 of the IL-1 zeta locus, and the encoded protein
 CC is probably a functional IL-1 like molecule. TD2.2 mRNA is expressed most
 CC strongly in the testis and bone marrow. The invention is directed to
 CC novel, purified and isolated IL-1 zeta, its splice variants and Xrec2
 CC polypeptides (see AAY9297-301), the nucleic acids (see AAA27918-22)
 CC encoding such polypeptides, processes for production of recombinant forms
 CC of such polypeptides, and their uses. The polypeptides can be used to
 CC study cellular processes such as immune regulation, cell proliferation,
 CC cell death, cell migration, cell-to-cell interaction, cell inflammatory
 CC responses, to identify proteins associated with IL-1 zeta, to screen for
 CC potential inhibitors, and to prepare antibodies. In particular, they can
 CC be used to activate and/or inhibit the activation of vascular endothelial
 CC cells and lymphocytes, induce and/or inhibit the induction of local
 CC tissue destruction and fever, inhibit and/or stimulate macrophages and
 CC vascular endothelial cells to produce IL-6, induce and/or inhibit the
 CC induction of prostaglandins, nitric oxide synthetase, and
 CC metalloproteinases, and upregulate and/or inhibit the upregulation of
 CC molecules on the surface of vascular endothelial cells
 CC
 CC Sequence 197 AA;
 XX
 SQ
 Query Match 85.2%; Score 902; DB 3; Length 197;
 Best Local Similarity 91.5%; Pred. No. 2.5e-95;
 Matches 172; Conservative 4; Mismatches 6; Indels 6; Gaps 1;
 QY 16 DYKDDDDKLAANGALGRPVKYNLPKFSIHQDQKVLVDSGNLAVDPKNYIRPEI 75
 DB 16 DWEDEDEQ-----CCLEGPVKYNLPKFSIHQDQKVLVDSGNLAVDPKNYIRPEI 69
 QY 76 FFALASSLSASAEKSPILVGSKEFCVCDKDGQSHPSIQLKKEKMLKLAQKESA 135
 DB 70 FFALASSLSASAEKSPILVGSKEFCVCDKDGQSHPSIQLKKEKMLKLAQKESA 129
 QY 136 RRPPIFRAQVGSNNMLESAAHPGFICTSCNENPEVGTDFENRKHIIEFSFPVCKAE 195
 DB 130 RRPPIFRAQVGSNNMLESAAHPGFICTSCNENPEVGTDFENRKHIIEFSFPVCKAE 189
 QY 196 MSPSEVSD 203
 DB 190 MSPSEVSD 197

XX Homo sapiens.
 OS
 XX WO200140247-A1.
 PN
 XX 07-JUN-2001.
 PD
 XX 30-NOV-2000; 2000MO-US032521.
 PF
 XX 01-DEC-1999; 99US-00452140.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA
 XX
 PI Kumar S, McDonnell PC, Young PR;
 XX
 DR WPI; 2001-389949/41.
 XX
 CC Novel interleukin-1 homolog, IL-1H4, for treating chronic and acute
 CC inflammation, septicemia, autoimmune diseases, transplant rejection,
 CC graft versus host disease, stroke, ischemia, allergy and asthma.
 CC
 CC Claim 1; Page 29; 30pp; English.
 XX
 PS The invention provides an isolated interleukin-1 homologue, IL-1H4
 CC polypeptide. The IL-1H4 polypeptide can be expressed by standard
 CC recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
 CC modulators are useful for treating chronic and acute inflammation,
 CC septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
 CC psoriasis and arthritis), transplant rejection, graft versus host
 CC disease, infection, stroke, ischemia, acute respiratory disease syndrome,
 CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
 CC osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
 CC heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
 CC polynucleotides are useful as diagnostic reagents and for chromosome
 CC identification. The present sequence represents the IL-1H4 mature
 CC polypeptide
 CC
 CC Sequence 198 AA;
 XX
 SQ
 Query Match 84.5%; Score 895; DB 4; Length 198;
 Best Local Similarity 100.0%; Pred. No. 1.6e-94;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 PKYKNLPKFSIHQDQKVLVDSGNLAVDPKNYIRPEIFPALASSLSASAEKSP 94
 DB 30 PKYKNLPKFSIHQDQKVLVDSGNLAVDPKNYIRPEIFPALASSLSASAEKSP 89
 QY 95 LIGVSKGEFCVCDKDGQSHPSIQLKKEKMLKLAQKESARRPFIYRAQVGSNNMLES 154
 DB 90 LIGVSKGEFCVCDKDGQSHPSIQLKKEKMLKLAQKESARRPFIYRAQVGSNNMLES 149
 QY 155 AAHPGFICTSCNENPEVGTDFENRKHIIEFSFPVCKAEMSPSEVSD 203
 DB 150 AAHPGFICTSCNENPEVGTDFENRKHIIEFSFPVCKAEMSPSEVSD 198

RESULT 5
 ID AAY96938 standard; protein; 207 AA.
 XX
 AC AAY96938;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Human IL-1 receptor antagonist 1 long.
 XX
 KW hIL-1Ralt; human interleukin-1 receptor antagonist-1 long; IL-1lp;
 KW osteopontin; interleukin-1-like polypeptide; anti-inflammatory;
 KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
 KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
 KW gene therapy.
 XX
 OS Homo sapiens.

PX		WNZ000039297-A2.	
PN			
XX			
PD		06-JUL-2000.	
XX			
PF	22-DEC-1999;	99WO-US030720.	
XX			
PR	23-DEC-1998;	98US-0113430P.	
PR	22-JAN-1999;	99US-0116843P.	
PR	13-APR-1999;	99US-0129122P.	
PA	(GETH) GENENTECH INC.		
PI	Goddard A, Pan J;		
DR	WPI: 2000-452395/39.		
DR	N-PSTDB; AAA51601.		
PS	Claim 22; Fig 15; 143pp; English.		
XX			
CC	An isolated nucleic acid molecule encoding an interleukin-1-like polypeptide (IL-1lp) that retains one or more activities of the peptide from which it is derived, such as the IL-18R binding activity of a human interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The nucleic acids may be used in molecular engineering applications, e.g. hybridization assays and chromosome and gene mapping studies, for recombinantly producing the IL-1lp polypeptide or for producing gene knock out animals to study the role of the protein in metabolism and disease processes (conversely, gene therapy protocols may be used to supplement a patient's production of the polypeptide or to rectify mutations that lead to the production of inactive peptides). The peptides produced may be used to screen for and produce modulators (e.g. antibodies) of IL-1lp protein expression and activity which may be used to treat disorders associated with inappropriate IL-1lp expression and activity, such as inflammatory disorders, asthma, arthritis, osteoarthritis, sepsis, acute lung injury, adult respiratory distress syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease, psoriasis, graft versus host disease and/or inflammatory bowel disease		
XX			
SQ	Sequence 207 AA;		
	Query Match	84.5%; Score 995; DB 3; Length 207;	
	Best Local Similarity	100.0%; Pred. No. 1.7e-94;	
	Matches 169; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	35 PKVKNLNLKKRSIHQDHRKVLVDSGNLIAVDKNYIRPEIFALASSLSASAEKGSP	I 94	
Db	39 PKVKNLNPKRRSHIDQHKLVLDGSLIAVPDKYIRPEIFALASSLSASAEKGSP	I 98	
QY	95 LLAGVSGEFCLCYCDKDGQSHPISIQLKKEKLMKLAAOKESARRPITFYRAQGVSNM	T 154	
Db	99 LLAGVSKGFCLCYCDKDGQSHPISIQLKKEKLMKLAAOKESARRPITFYRAQGVSNM	T 158	
QY	155 AAHGGMFICTSCNCPNPVGYNDDKPPNRGHIEFSFPVCKAEMSPSEVSD	D 203	
Db	159 AAHGGMFICTSCNCPNPVGVTDKTENRKHIIEFSFPVCKAEMSPSEVSD	D 207	
	RESULT 6		
XX	AAAY70927		
XX	ID	AAAY70927 standard; protein, 218 AA.	
XX	AC	AAAY70927;	
DT	05-SEP-2000	(first entry)	
XX			
DE	Human zllaa4 protein.		
XX			
TM	Human interleukin-1; IL-1; zllaa4 protein; inflammation; arthritis; perioritis; septic shock; graft-versus-host disease; leukaemia; cancer		

XX	Homo sapiens.	
OS		
KW	anemia; inflammatory bowel disease; acute neuropathology; shock;	
KW	chronic neuropathology; respiratory disease syndrome; restenosis;	
KW	acquired immune deficiency syndrome; AIDS; anti-inflammatory; cytostatic	
KW	anti-arthritic; anti-psoriatic; antibacterial; immunosuppressive;	
KW	anti-anemic; neuroprotective; vasotropic;	
KW	anti-human immunodeficiency virus; HIV.	
XX		
XX	Location/Qualifiers	
FT	Key	
FT	Domain	60..64
FT	Domain	/label= Beta_strand
FT	Domain	65..67
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	68..72
FT	Domain	/label= Beta_strand
FT	Domain	73..76
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	77..79
FT	Domain	/label= Beta_strand
FT	Domain	80..89
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	90..96
FT	Domain	/label= Beta_strand
FT	Domain	97..107
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	108..113
FT	Domain	/label= Beta_strand
FT	Domain	114..117
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	118..123
FT	Domain	/label= Beta_strand
FT	Domain	124..131
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	132..138
FT	Domain	/label= Beta_strand
FT	Domain	139..153
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	154..160
FT	Domain	/label= Beta_strand
FT	Domain	161..164
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	165..169
FT	Domain	/label= Beta_strand
FT	Domain	170..174
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	175..179
FT	Domain	/label= Beta_strand
FT	Domain	180..186
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	187..189
FT	Domain	/label= Beta_strand
FT	Domain	190..200
FT	Domain	/note= "Variable loop region involved in receptor binding"
FT	Domain	201..204
FT	Domain	/label= Beta_strand
XX		
XX	WO200024899-A2.	
XX		
XX	04-MAY-2000.	
XX		
XX	27-OCT-1999;	99WO-US025038.
XX		

XX 27-OCT-1998; 98US-00179614.
 PR (ZYMO) ZYMOGENETICS INC.
 XX
 PA West RR, Sheppard PO, Gao Z;
 PI WPI; 2000-350740/30.
 DR N-PSDB; AAD00210.
 XX
 XX Immunomodulatory interleukin-1 homolog zila4 proteins, useful for
 PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
 PT disease, leukemia.
 XX
 XX Claim 4; Fig 2; 88pp; English.
 PS
 XX The present sequence is the human interleukin (IL)-1 homolog zila4
 CC protein. This protein contains a core structure of 12 beta-strands wound
 CC into a beta-barrel, with the beta-strands separated from each other by
 CC loops. The loops between these beta-strands are highly variable among the
 CC family members and are believed to be involved in receptor binding. The
 CC zila4 proteins modulate inflammation and other immunological processes
 CC and are therefore useful for treatment of arthritis, psoriasis, septic
 CC shock, graft-versus-host disease and leukemia. Other diseases that may
 CC be modulated by zila4 proteins include cancer, anaemia, inflammatory
 CC bowel disease, acute and chronic neuropathologies, shock, respiratory
 CC disease syndrome, restenosis and acquired immune deficiency syndrome
 CC
 SQ Sequence 218 AA;
 Query Match 84.5%; Score 895; DB 3; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1.9e-94;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 PKYKNLNPKKFSIHDDQHKVLDLSDGNLAVDPKNYIRPEIFPALASSLSASAEKGSPI 94
 DB 50 PKYKNLNPKKFSIHDDQHKVLDLSDGNLAVDPKNYIRPEIFPALASSLSASAEKGSPI 109
 QY 95 LLAGVSKGEFLCYCDKXGSHPSLQKKKELMKLAQKESARRPFIYRAQVGSMMNLES 154
 DB 110 LLAGVSKGEFLCYCDKXGSHPSLQKKKELMKLAQKESARRPFIYRAQVGSMMNLES 169
 QY 155 AAHPGFICTSCNCPNCPVGTDFENRKHIEFSFQPCAKEMSPSEVSD 203
 DB 170 AAHPGFICTSCNCPNCPVGTDFENRKHIEFSFQPCAKEMSPSEVSD 218
 RESULT 7
 ID AAY91885 standard; protein: 218 AA.
 XX
 AC AAY91885;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Primate interleukin-1 like molecule (IL-1-zeta) alternative sequence.
 XX
 KW Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever;
 KW hypoglycemia; plasma iron; plasma zinc; acute liver response;
 KW plasma copper.
 XX
 OS Mammalia.
 XX
 PH Key Location/Qualifiers
 FT Domain /label= beta_strand_1
 FT Domain /label= beta_strand_2
 FT Domain /label= beta_strand_3
 FT Domain /label= beta_strand_4
 FT Binding-site /label= beta_strand_4

FT /note= "forms a loop which is part of a primary binding
 FT segment to the IL-1 receptor type"
 FT
 FT Domain
 FT /label= beta_strand_5
 FT Domain
 FT /label= beta_strand_6
 FT Domain
 FT /label= beta_strand_7
 FT Domain
 FT /label= beta_strand_8
 FT Domain
 FT /label= beta_strand_9
 FT Domain
 FT /label= beta_strand_10
 FT Domain
 FT /label= beta_strand_11
 FT Domain
 FT /label= beta_strand_12
 XX
 XX WO200017363-A2.
 XX
 XX 30-MAR-2000.
 XX
 XX 17-SEP-1999; 99WO-US020868.
 XX
 XX 18-SEP-1998; 98US-00156966.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Timans JC;
 XX
 XX WPI; 2000-283588/24.
 XX
 XX N-PSDB; AAA08513.
 DR
 XX
 XX New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful
 PT for diagnostic and therapeutic purposes, comprises a 128 amino acid
 PT sequence.
 PT
 XX
 XX Claim 1; Page 103-104; 110pp; English.
 PS
 XX
 XX The present sequence is an alternative primate interleukin-1 like
 CC molecule, designated IL-1-zeta. The 12 beta strands, indicated in the
 CC features table, fold into a beta-trefoil fold. The specification claims
 CC an isolated or recombinant polypeptide that: (a) specifically binds
 CC polyclonal antibodies generated against at least a 12 consecutive amino
 CC acid segment of IL-1-zeta (see AAY91884) or its allelic variant (see
 CC AAY91885); and (b) comprises at least one sequence selected from:
 CC AAY91886-903 or AAY91904-06. The preferred 12 consecutive amino acid
 CC segment is chosen from AAY91907-18 or AAY91919-21. IL-1-zeta is likely to
 CC play a role in systemic inflammatory reactions, such as fever,
 CC hypoglycemia, reduced plasma iron and zinc, the acute response of the
 CC liver, and increase plasma copper. IL-1-zeta binding compounds
 CC (comprising antigen binding sites) and IL-1-zeta polypeptides are also
 CC useful for both diagnostic and therapeutic purposes
 CC
 SQ Sequence 218 AA;
 Query Match 84.5%; Score 895; DB 3; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1.9e-94;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 PKYKNLNPKKFSIHDDQHKVLDLSDGNLAVDPKNYIRPEIFPALASSLSASAEKGSPI 94
 DB 50 PKYKNLNPKKFSIHDDQHKVLDLSDGNLAVDPKNYIRPEIFPALASSLSASAEKGSPI 109
 QY 95 LLAGVSKGEFLCYCDKXGSHPSLQKKKELMKLAQKESARRPFIYRAQVGSMMNLES 154
 DB 110 LLAGVSKGEFLCYCDKXGSHPSLQKKKELMKLAQKESARRPFIYRAQVGSMMNLES 169
 QY 155 AAHPGFICTSCNCPNCPVGTDFENRKHIEFSFQPCAKEMSPSEVSD 203
 DB 170 AAHPGFICTSCNCPNCPVGTDFENRKHIEFSFQPCAKEMSPSEVSD 218

XX	AAAY95299	standard; protein; 218 AA.
XX	AAAY95299	
XX	AAAY95299;	
DT	12-SEP-2000	(first entry)
XX		
DE		Human interleukin-1 zeta splice variant TDZ.1.
XX		
KW		Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.1;
KW		testis-derived zeta variant; therapy; inflammation; fever.
XX		
OS		Homo sapiens.
XX		
PN	WO2000036108-A2.	
XX		
PD	22-JUN-2000.	
XX		
PF	14-DEC-1999;	99WO-US029549.
XX		
PR	14-DEC-1998;	98US-0112163P.
PR	10-NOV-1999;	99US-0164675P.
XX		
PA	(IMMV) IMMUNEX CORP.	
XX		
PI	Sims JE, Smith DE, Born TL;	
XX		
DR	WPI; 2000-442387/38.	
DR	N-PSDB; AAA27920.	
XX		
PT		Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT	TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for	
PT	identifying genes associated with diseases such as glaucoma, and insulin-	
PT	dependent diabetes mellitus.	
XX		
XX		
XX	Claim 10; Page 11; 87pp; English.	
XX		
CC	The present sequence is that of splice variant TDZ.1 (testis-derived zeta	
CC	variant) of human interleukin-1 zeta (IL-1 zeta). TDZ.1 mRNA is generated	
CC	from exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus, and the encoded	
CC	protein is probably a functional IL-1 like molecule. TDZ.1 mRNA is	
CC	expressed most strongly in the kidney, skeletal muscle, testis, prostate,	
CC	ovary, colon, small intestine, liver, placenta, lung, tonsil, foetal	
CC	liver, lymph node and bone marrow. The invention is directed to novel,	
CC	purified and isolated IL-1 zeta, its splice variants and Xrec2	
CC	polypeptides (see AAAY95297-301), the nucleic acids (see AAA27918-22)	
CC	encoding such polypeptides, processes for production of recombinant forms	
CC	of such polypeptides, and their uses. The polypeptides can be used to	
CC	study cellular processes such as immune regulation, cell proliferation,	
CC	cell death, cell migration, cell-to-cell interaction and inflammatory	
CC	responses, to identify proteins associated with IL-1 zeta, to screen for	
CC	potential inhibitors, and to prepare antibodies. In particular, they can	
CC	be used to activate and/or inhibit the activation of vascular endothelial	
CC	cells and lymphocytes, induce and/or inhibit the induction of local	
CC	tissue destruction and fever, inhibit and/or stimulate macrophages and	
CC	vascular endothelial cells to produce IL-6, induce and/or inhibit the	
CC	induction of prostaglandins, nitric oxide synthetase, and	
CC	metalloproteinases, and upregulate and/or inhibit the upregulation of	
CC	molecules on the surface of vascular endothelial cells	
XX		
XX	Sequence 218 AA;	

Query Match	84.5%	Score 895	DB 3	Length 218
Best Local Similarity	100.0%	Pred. No.	1.9e+94	
Matches 169	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 95 ILGYSKGEFLCYCDKDGQSHPSLQKKEKMLKLAQKESARPRFTFYAAGVGNMLES 154

Db	Qy
110	110 LLGSGKGFCLCYCDKDKQGSHPSTQLKKKKKMLAKQKESARPEIPIYRAQGVGSMNLTSS 169
155	155 AAHRCWFLCTSCNCNPEVGYTDKCKENRKGIRPESFPQVCKAKMSPEVSD 203
170	170 AAHRCWFLCTSCNCNPEVGYTDKCKENRKGIRPESFPQVCKAKMSPEVSD 218

RESULT 9
AAY96940
ID AAY96940 standard; protein; 218 AA.

DT 31-OCT-2000 (first entry)

DE Human IL-1 receptor antagonist 1 V.
XY

KW hIL-1RA1V; human interleukin-1 receptor antagonist-1; IL-1p;

KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;

anti-ischemic; immunomodulatory; gastroenteric; gene therapy.

2000

PN WO2000039297-A2

06-JUL-2000

PF 22-DEC-1999; 99WO-US030720

23-DEC-1998: 98US-0113430P

PR 22-JAN-1999; 99US-0116843P
PR 13-APR-1999; 99US-0138133P

XX
XX
(continued)

XX

XX
FI Gouard A, Fall C,
XX

DR WPI; 2000-452395/39.
 DP N-PSDB; AAA51604

PT Nucleic acids encoding interleukin-1-like polypeptides, useful for preventing and treating e.g. inflammation, asthma and psoriasis.

PS Claim 22; Fig 19; 143pp; English.

CC An isolated nucleic acid molecule encoding an interleukin-1-like

polypeptide (IL-11p) that retains one or more activities of the peptide from which it is derived, such as the IL-18R binding activity of a human

CC interleukin-1 receptor antagonist-1 (hIL-1RAc1) polypeptide, is new. The

CC hybridization assays and chromosome and gene mapping studies, for

knock out animals to study the role of the protein in metabolism and

CC disease processes (conversely, gene therapy protocols may be used to supplement a patient's production of the polypeptide or to rectify CC

mutations that lead to the production of inactive peptides). The

CC antibodies) of IL-11p protein expression and activity which may be used

activity, such as inflammatory disorders, asthma, arthritis,

CC osteoarthritis, beryllium, acute lung injury, adult respiratory distress syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease

CC psoriasis, graft versus host disease and/or inflammatory bowel disease

SQ Sequence 218 AA;

Query Match	84.5%	Score	835	DB 3	length	218	
Best local similarity	100.0%	Pred. No.	1	9e-94			
Matches	169	Conservative	0	Mismatches	0	Gaps	0

```
OY 35 PKVKNLPPKFFSIHDDHKVLVLDGSLIAPDKNYIRPEIFPALASSLSASAEKGSPI 94
DB 50 PKVKNLPPKFFSIHDDHKVLVLDGSLIAPDKNYIRPEIFPALASSLSASAEKGSPI 109
OY 95 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMNLES 154
DB 110 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMNLES 169
OY 155 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPVCKAEMSPSEVSD 203
DB 170 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPVCKAEMSPSEVSD 218

RESULT 10
AAB28266
ID AAB28266 standard; protein; 218 AA.
AC
XX AAB28266;
XX
XX 13-FEB-2001 (first entry)
XX
XX Human interleukin-1 homologue IL-1H4.
XX
XX Human, interleukin-1 homologue; IL-1H4; inflammation; septicemia;
XX autoimmune disease; inflammatory bowel disease; psoriasis; arthritis;
XX transplant rejection; graft versus host disease; infection; stroke;
XX ischaemia; acute respiratory disease; allergy; asthma; restenosis;
XX brain injury; AIDS; bone disease; osteoporosis; cancer;
XX congestive heart failure; atherosclerosis; Alzheimer's disease.
XX
XX Homo sapiens.
XX
XX W0200063226-A1.
XX
XX 26-OCT-2000.
XX
XX 14-APR-2000; 2000WO-US010207.
XX
XX 16-APR-1999; 99US-00293625.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Young PR, McDonnell PC;
XX
XX WPI; 2000-687155/67.
XX
XX N-PSDB; AAC66727.
XX
XX Interleukin-1 homolog useful for treating conditions such as chronic and
XX acute inflammation, septicemia, autoimmune diseases ischemia, acute
XX respiratory disease, allergies, and asthma.
XX
XX Claim 1; Page 28-29; 30pp; English.
XX
XX The present sequence is human interleukin-1 homologue (IL-1H4). IL-1H4 is
XX useful for treating conditions such as chronic and acute inflammation,
XX septicemia, autoimmune diseases (e.g. inflammatory bowel disease,
XX psoriasis, and arthritis), transplant rejection, graft versus host
XX disease, infection, stroke, ischaemia, acute respiratory disease,
XX allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.
XX osteoporosis), cancer, congestive heart failure, atherosclerosis, and
XX Alzheimer's disease, related to either an excess of, or an under-
XX expression of, IL-1H4 polypeptide activity
XX
XX Sequence 218 AA;
XX
XX Query Match 84.5%; Score 895; DB 3; Length 218;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-94;
XX Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 35 PKVKNLPPKFFSIHDDHKVLVLDGSLIAPDKNYIRPEIFPALASSLSASAEKGSPI 94
DB 50 PKVKNLPPKFFSIHDDHKVLVLDGSLIAPDKNYIRPEIFPALASSLSASAEKGSPI 109
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OY 95 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMNLES 154
DB 110 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMNLES 169
OY 155 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPVCKAEMSPSEVSD 203
DB 170 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPVCKAEMSPSEVSD 218
```

```
RESULT 11
AAB47186
ID AAB47186 standard; protein; 218 AA.
AC
XX AAB47186;
XX
XX 29-JUN-2001 (first entry)
XX
XX IL-1 related polypeptide.
XX
XX Interleukin-1-related polypeptide; HPB-MLT cell; T-cell; inhibition;
XX natural killer activity; immune system; gene therapy; immunodeficiency.
XX
XX Homo sapiens.
XX
XX EP1092773-A2.
XX
XX 18-APR-2001.
XX
XX 11-OCT-2000; 2000EP-00308948.
XX
XX 15-OCT-1999; 99JP-00294493.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Ushio S, Mukada Y, Yamamoto K, Kurimoto M;
XX
XX WPI; 2001-275206/29.
XX
XX N-PSDB; AAC65680.
XX
XX New human interleukin-1-related polypeptide and polynucleotide, useful
XX for gene therapy and in developing drugs as regulators of natural killer
XX activity, are capable of inhibiting natural killer activity.
XX
XX Claim 1; Page 12; 15pp; English.
XX
XX This sequence represents an interleukin-1 (IL-1)-related polypeptide. IL-
XX 1 related polypeptide was isolated from HPB-MLT cells, FERM-BP-2430, an
XX established human T-cell line. IL-1 related polypeptide is useful for
XX inhibiting natural killer (NK) activity, which is related to the immune
XX system of mammals. The DNA encoding the IL-1 related polypeptide is
XX useful in gene therapy of patients in need of NK activity inhibition and
XX others suffering from immunodeficiency
XX
XX Sequence 218 AA;
XX
XX Query Match 84.5%; Score 895; DB 4; Length 218;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-94;
XX Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 35 PKVKNLPPKFFSIHDDHKVLVLDGSLIAPDKNYIRPEIFPALASSLSASAEKGSPI 94
DB 50 PKVKNLPPKFFSIHDDHKVLVLDGSLIAPDKNYIRPEIFPALASSLSASAEKGSPI 109
OY 95 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMNLES 154
DB 110 LLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMNLES 169
OY 155 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPVCKAEMSPSEVSD 203
DB 170 AAHPGFICTSCNCPNEPVGVTDKFENRKHIEFSFPVCKAEMSPSEVSD 218

RESULT 12
```

ID	AAG68116
AC	AAG68116 standard; protein; 218 AA.
XX	
DT	22-JAN-2002 (first entry)
DE	Human interleukin 1 family protein SEQ ID NO:2.
XX	
KM	Human: interleukin 1; IL-1; growth factor; Tango-77; diagnosis;
KW	identification.
OS	Homo sapiens.
PB	JF2001231578-A.
PD	28-Aug-2001.
PF	07-Dec-2000; 2000JP-00372864.
PR	09-Dec-1999; 99JP-00349780.
PA	(KYOW) KYOWA HAKKO KOGYO KK.
DR	WPJ; 2001-609968/70.
N-PSDB:	AAI71179.
PT	An IL-1 family protein, used for the development of diagnostic and treatment agents.
PS	Claim 1; Page 30; 38pp; Japanese.
CC	The present sequence represents a human interleukin 1 (IL-1) family protein having a combining affinity to a receptor of a protein of human IL-1 family higher than Tango-77. The protein is useful for the development of diagnostic, treating and/or preventive agents for various diseases
SQ	Sequence 218 AA;
Query Match	84.5%; Score 895; DB 4; Length 218; Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches	169; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Df	35 PKVKNLNPKEFSIHDDHKVLVLDSGNTIAVPDKYIRPEIFPALASSISASAEGSBI 94 50 PKVNLNLPKKSIIHQDHRKVLVDGNDLIAVPDKYIRPEIFFALASSISSASAEKGSP 109
Dd	95 LLGVSKGEFCYCYPDXDGSHPSIQLKKKEXLMKLAAOKESARRPFIFFRAOVGSNNML 154 110 LLAGVGSEFCCLCDXDGSHPSIDQLKKRCKMKLAOKESAARRPIFFRAOVGSNNML 169
Dy	155 AADRGMPICITSCNCNEPVGVTDFENRKHIIEFSFPVCKAEMSPEVSVD 203 170 AAHGWMFICTSCNCNEPVGVTDFENRHGIIEFSFPVCKAEMSPESVSD 218
R	RESULT 13
ID	AAB85136
AC	AAB85136 standard; protein; 218 AA.
XX	
DT	22-AUG-2001 (first entry)
DE	Interleukin-1 homologue (IL-1H4) polypeptide.
XX	
KM	Interleukin-1; IL-1H4; anti-inflammatory; antibacterial; antiallergic;
KW	immunosuppressive; antisporadic; antiarthritis; cytostatic; anti-HIV;
KM	cerebroprotective; asthmatic; vasotrophic; vulnaray; osteopathic;
KW	immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;
KW	gene therapy; vaccine.
XX	

OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..20
FT		/note= "signal peptide"
FT	Cleavage-site	20..21
FT	Protein	21..218
FT		/note= "specifically claimed mature protein (AAB85138)"
XX		
PN	MO2001.40247-A1.	
XX		
PD	07-JUN-2001.	
XX		
XX	30-NOV-2000; 2000WO-US032521.	
PF		
XX	01-DEC-1999; 99US-00452140.	
PR		
XX		
PA	(SMIK) SMITHKLINE BEECHAM CORP.	
PI	Kumar S, McDonnell PC, Young PR;	
XX		
DR	WPI: 2001-389949/41.	
DR	N-PSDB; AAF64120.	
XX		
XX	Novel Interleukin-1 homolog, IL-1H4, for treating chronic and acute	
PT	inflammation, septicemia, autoimmune diseases, transplant rejection,	
PT	graft versus host disease, stroke, ischemia, allergy and asthma.	
XX		
PS	Example; Page 29; 30pp; English.	
XX		
CC	The invention provides an isolated interleukin-1 homologue, IL-1H4	
CC	polypeptide. The IL-1H4 polypeptide can be expressed by standard	
CC	recombinant methodology. The IL-1H4 polypeptide, polynucleotides and	
CC	modulators are useful for treating chronic and acute inflammation,	
CC	septicemia, autoimmune diseases (e.g., inflammatory bowel disease,	
CC	psoriasis and arthritis), transplant rejection, graft versus host	
CC	disease, infection, stroke, ischemia, acute respiratory disease syndrome,	
CC	allergies, asthma, resectosis, brain injury, AIDS, bone diseases (e.g.,	
CC	osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive	
CC	heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4	
CC	polynucleotides are useful as diagnostic reagents and for chromosome	
CC	identification. The present sequence represents the IL-1H4 polypeptide	
XX		
SO	Sequence 218 AA;	
	Query Match	84.5%; Score 895; DB 4; Length 218;
	Best Local Similarity	100.0%; Pred. No. 1.9e-94;
	Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	35 PKYNNLPKPPSHIHDDHKLVLVDSGULIAPDPKNYIRPEIFFLASSLSASAEKSP	94
DB	50 PKYNNLPKPPSHIHDDHKLVLVDSGULIAPDPKNYIRPEIFFLASSLSASAEKSP	109
QY	95 ILGVSKPEFLCYCDKDGKSGHPSQLKKKELKMLAOKESARRPFIFYRAQVGSMN	154
DB	110 ILGVSKPEFLCYCDKDGKSGHPSQLKKKELKMLAOKESARRPFIFYRAQVGSMN	169
QY	155 AAPHGWFITCSNCNNEPVGVTDKRENRKHIFESFQPVCKAEMSGSEVSD	203
DB	170 AAPHGWFITCSNCNNEPVGVTDKRENRKHIFESFQPVCKAEMSGSEVSD	218
	RESULT 14	
	ID AAY71084 standard; protein; 218 AA.	
XX	AA71084;	
XX	AC	
XX	05-SEP-2000 (first entry)	
DE	Human z11a4-E200D variant protein.	
XX	Human interleukin-1; IL-1; z11a4 protein; inflammation; arthritis;	

psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
anemia; inflammatory bowel disease; acute neuropathology; shock;
chronic neuropathology; respiratory disease syndrome; resectosis;
acquired immune deficiency syndrome; AIDS; anti-inflammatory; cytostatic;
anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
anti-naemic; neuroprotective; vasotropic; variant;
anti-human immunodeficiency virus; HIV.

OS Homo sapiens.
XX
XX WO200024899-A2.
XX
XX 04-MAY-2000.
XX
XX 27-OCT-1999; 99WO-US025038.
XX
XX 27-OCT-1998; 98US-00179614.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX West RR, Sheppard PO, Gao Z;
XX WPI; 2000-350740/30.
XX
XX Immunomodulatory interleukin-1 homolog zll1a4 proteins, useful for
PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
PT disease, leukemia.
XX
XX Claim 3; Page; 88pp; English.

CC The present sequence is a variant of human interleukin (IL)-1 homolog
CC zll1a4 protein, consisting of Asp in place of Glu at position 200. The
CC replacement of Glu (200) with Asp results in attenuation of pro-
CC inflammatory activity of zll1a4 protein. The zll1a4 proteins modulate
CC inflammation and other immunological processes and are therefore useful
CC for treatment of arthritis, psoriasis, septic shock, graft-versus-host
CC disease and leukaemia. Other diseases that may be modulated by zll1a4
CC proteins include cancer, anaemia, inflammatory bowel disease, acute and
CC chronic neuropathologies, shock, respiratory disease syndrome, resectosis
CC and acquired immune deficiency syndrome. Note: The present sequence is
CC not shown in the specification but is derived from human zll1a4 protein
CC sequence shown in figure-2 (AAV70927)
XX
XX

SO Sequence 218 AA;
Query Match 84.2%; Score 892; DB 3; Length 218;
Best Local Similarity 99.4%; Pred. No. 4.2e-94;
Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVKNLPPKKESTHDDHKLVLDSGNLIVDPKNYIRPEIFPALASSLSASAEKSGSPI 94
DB 50 PKVKNLPPKKESTHDDHKLVLDSGNLIVDPKNYIRPEIFPALASSLSASAEKSGSPI 109
QY 95 LLAGVSKGEFCLYCDKDGQSHPSLQKKERKMLAAQKESARRPFIFRYAOGVGMNMLE 154
DB 110 LLAGVSKGEFCLYCDKDGQSHPSLQKKERKMLAAQKESARRPFIFRYAOGVGMNMLE 169
QY 155 AAHPGWFICTSCNENPEVGTDKFENRKHIEFSQPVCKAEMSPSEVSD 203
DB 170 AAHPGWFICTSCNENPEVGTDKFENRKHIDFSQPVCKAEMSPSEVSD 218

RESULT 15
AAV70933
ID AAV70933 standard; protein; 218 AA.
XX
XX AAV70933;
XX
XX 05-SEP-2000 (first entry)
XX
XX Human zll1a4-E200K variant protein.
XX
XX Human interleukin-1, IL-1; zll1a4 protein; inflammation; arthritis;

psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
anemia; inflammatory bowel disease; acute neuropathology; shock;
chronic neuropathology; respiratory disease syndrome; resectosis;
acquired immune deficiency syndrome; AIDS; anti-inflammatory; cytostatic;
anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
anti-naemic; neuroprotective; vasotropic;
anti-human immunodeficiency virus; HIV.

OS Homo sapiens.
XX
XX WO200024899-A2.
XX
XX 04-MAY-2000.
XX
XX 27-OCT-1999; 99WO-US025038.
XX
XX 27-OCT-1998; 98US-00179614.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX West RR, Sheppard PO, Gao Z;
XX WPI; 2000-350740/30.
XX
XX N-PSDB; AAD00212.
XX
XX Immunomodulatory interleukin-1 homolog zll1a4 proteins, useful for
PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
PT disease, leukemia.
XX
XX Claim 8; Page 77-78; 88pp; English.

CC The present sequence is a variant of human interleukin (IL)-1 homolog
CC zll1a4 protein designated zll1a4-E200K. The replacement of Glu (200) with
CC Lys results in change in activity from agonist to antagonist. The zll1a4
CC proteins modulate inflammation and other immunological processes and are
CC therefore useful for treatment of arthritis, psoriasis, septic shock,
CC graft-versus-host disease and leukaemia. Other diseases that may be
CC modulated by zll1a4 proteins include cancer, anaemia, inflammatory bowel
CC disease, acute and chronic neuropathologies, shock, respiratory disease
CC syndrome, resectosis and acquired immune deficiency syndrome
XX
XX

SO Sequence 218 AA;
Query Match 84.1%; Score 891; DB 3; Length 218;
Best Local Similarity 99.4%; Pred. No. 5.4e-94;
Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVKNLPPKKESTHDDHKLVLDSGNLIVDPKNYIRPEIFPALASSLSASAEKSGSPI 94
DB 50 PKVKNLPPKKESTHDDHKLVLDSGNLIVDPKNYIRPEIFPALASSLSASAEKSGSPI 109
QY 95 LLAGVSKGEFCLYCDKDGQSHPSLQKKERKMLAAQKESARRPFIFRYAOGVGMNMLE 154
DB 110 LLAGVSKGEFCLYCDKDGQSHPSLQKKERKMLAAQKESARRPFIFRYAOGVGMNMLE 169
QY 155 AAHPGWFICTSCNENPEVGTDKFENRKHIEFSQPVCKAEMSPSEVSD 203
DB 170 AAHPGWFICTSCNENPEVGTDKFENRKHIDFSQPVCKAEMSPSEVSD 218

Search completed: September 9, 2004, 13:25:12
Job time : 127 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:19:49 / Search time 117 Seconds
(without alignments)
547.438 Million cell updates/sec

Title: US-09-869-566-5
Perfect score: 1059
Sequence: 1 MSALLILALVGAADVADYKD.....IEFSFQVCKAEMSEFSEVSD 203

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

SPREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	16.3	159	11	Q8CGA1
2	158.5	15.0	159	4	Q96GD6
3	152.5	14.4	267	13	Q73909
4	151	14.3	176	6	Q9BEH0
5	150	14.2	177	6	Q9GDM2
6	148.5	14.0	272	13	Q9DDP2
7	148	14.0	177	6	Q866R8
8	145.5	13.7	272	13	Q8AXV9
9	141	13.3	176	6	Q9GKX2
10	137.5	13.0	272	13	Q9DDP3
11	136	12.8	273	13	Q7T056
12	129.5	12.2	276	13	Q57398
13	129.5	12.2	276	13	Q9PW18
14	128.5	12.1	238	13	Q8AXV8
15	128	12.1	267	6	Q29082
16	125	11.8	211	6	Q7YS41

17	120.5	11.4	599	11	Q91WP7	Q91WP7 mus musculus
18	115.5	10.9	260	13	Q8U0J3	Q8U0J3 oncorhynch
19	115.5	10.9	260	13	Q9YGD3	Q9YGD3 oncorhynch
20	112	10.6	266	6	Q9TKL1	Q9TKL1 tursiops tr
21	112	10.6	266	6	Q8WNR2	Q8WNR2 delphinapte
22	112	10.6	301	13	Q802S3	Q802S3 scylliorhinu
23	111.5	10.5	247	13	Q8QGW0	Q8QGW0 paralicthy
24	109.5	10.3	246	13	Q98SG5	Q98SG5 scophthalmu
25	108	10.2	267	6	Q865X8	Q865X8 lama glama
26	107.5	10.2	302	13	Q7ZZK0	Q7ZZK0 triakis scy
27	107	10.1	72	6	Q77771	Q77771 equus caball
28	107	10.1	283	13	Q9PVZ5	Q9PVZ5 xenopus lae
29	106.5	10.1	254	13	Q9PT12	Q9PT12 oncorhynch
30	101.5	9.6	267	11	Q91ZL5	Q91ZL5 sigmodon hi
31	101	9.5	253	13	Q90W32	Q90W32 sparus aura
32	98	9.3	193	6	Q8HXK5	Q8HXK5 pan troglod
33	97.5	9.2	261	13	Q90W84	Q90W84 dicentrarch
34	94.5	8.9	269	6	Q8MKH3	Q8MKH3 salmistr sci
35	92	8.7	246	11	Q921R9	Q921R9 mus musculu
36	91	8.6	253	13	Q7ZZC7	Q7ZZC7 pagrus majo
37	89.5	8.5	153	4	Q43645	Q43645 homo sapien
38	88.5	8.4	152	6	Q8HXK6	Q8HXK6 macaca fasc
39	87.5	8.3	1201	16	Q7UYR6	Q7UYR6 rhodopirell
40	86.5	8.2	327	16	Q8A6K8	Q8A6K8 bacteroides
41	84.5	8.0	956	11	Q8VIG0	Q8VIG0 mus musculu
42	84	7.9	161	11	Q62161	Q62161 mus musculu
43	84	7.9	246	11	Q9ROT7	Q9ROT7 mus musculu
44	83.5	7.9	776	3	Q99287	Q99287 saccharomyc
45	83	7.8	246	11	Q9Q0K9	Q9Q0K9 mus musculu

ALIGNMENTS

RESULT 1

Q8CGA1 ID Q8CGA1 PRELIMINARY, PRT, 159 AA.
AC Q8CGA1
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Interleukin 1 receptor antagonist.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Strauberg R;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042532; AA042532.1;
DR GO; GO:0005176; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KM Receptor.
SQ SEQUENCE 159 AA; 17995 MW; BCA081C172903367 CRC64;

Query Match 16.3%; Score 173; DB 11; Length 159;

Best Local Similarity 37.1%; Pred. No. 1.9e-09;

Matches 53; Conservative 25; Mismatches 75; Indels 12; Gaps 7;
QY 27 ANSALCRGPVKVKNIPKFSIHDDHRYLVDSGNLIAYDPKNIYR-PEIFPALASSLS 85
DB 2 ASEAACRPSGRPCQKQAFRIWDTNGKTFYLRNNQLIA---GYLQSPNI--KLEEKLD 55

QY	86	ASAKGSGPILLVGSGEEFCVCDKDGSHPSLQKKEKLMKLAQKESARRPFIYRAQ	145
Db	56	VPIDLHS-VELGHHGKRLCLCSAKSGDDI--KLQLEENVITDLSKKEEDKR-FPIIRSE	111
QY	146	VGSWMMLESAHPGWFICTSCNCPNPVGTDKFENRKHI-EFSFQ	189
Db	112	KGPFTSPESAACPGWFLCTTLEADRPVSLTNPPEPLVTKRYFQ	156

RESULT 2

ID	Q96GD6	PRELIMINARY;	PRT;	159	AA.
AC	O96GD6;				
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE	Interleukin 1 receptor antagonist.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Pancreas;				
RA	Strauberg R.;				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC009745; AAH09745.1; -				
DR	PIR; I37893; A39386.				
DR	GO; GO:0005576; C:extracellular; IEA.				
DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
DR	GO; GO:0006955; P:immune response; IEA.				
DR	InterPro; IPR008996; Cytok_IL1_like.				
DR	InterPro; IPR000975; Interleukin_1.				
DR	Pfam; PF00340; IL1; 1.				
DR	ProDom; PD002536; Interleukin_1; 1.				
DR	SMART; SM0125; IL1; 1.				
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.				
KW	Receptor.				
SQ	SEQUENCE 159 AA; 17888 MW; CID6CDPDD2F7B44 CRC64;				

Query Match 15.0%; Score 158.5; DB 4; length 159;
 Best Local Similarity 29.1%; Pred. No.5.6e-08;
 Matches 44; Conservative 29; Mismatches 67; Indels 11; Gaps 6

QY	27	ANSALCRGPKYKNLNPKKFSIHDODHKVLVDSGNLIVDPDKYIR-DEIFALASSISS	85
Db	2	ALEETICRSGSKSSSMQAFRIMDVNQKTFYLRNNQVLA-----GYIGQPNV--NLEEKIDV	55
QY	86	ASAEKGSFILLGVSGEEFCVCDKDGSHPSLQKKEKLMKLAQKESARRPFIYRAQ	145
Db	56	VPIRPHA-LPIGHHGKWLCLCSVSGDETR--LQLEAVNITDLSNRKQDKR-FAFIRSD	111
QY	146	VGSWMMLESAHPGWFICTSCNCPNPVGTD 176	
Db	112	SGPFTSPESAACPGWFLCTTLEADRPVSLTN 142	

RESULT 3

ID	Q73909	PRELIMINARY;	PRT;	267	AA.
AC	O73909;				
DT	01-AUG-1998	(TREMBLrel. 07, Created)			
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE	Interleukin-1BETA.				
GN	IL-1BETA OR IL1B.				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianine;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				

RP	SEQUENCE FROM N.A.
RA	Weining K.C.; Sick C., Keepers B., Staeheli P.; et al.
RL	Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Line N;
RA	Kaiser J., Rothwell L., Goodchild M., Bumstead N.;
RT	"Chicken interleukin-1b: an evolutionary bridge between fish and mammals."
RL	Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; Y15006; CAAT5239.1; '-'
DR	EMBL; AJ245728; CAC04510.1; '-'
DR	HSSP; PI8510; IILR
DR	GO; GO:0005576; C:extracellular; IEA
DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA
DR	GO; GO:0006955; P:immune response; IEA
DR	GO; GO:0006954; P:inflammatory response; IEA
DR	InterPro; IPR008996; CytoK IL1 like.
DR	InterPro; IPR003502; IL1_propep_1.
DR	InterPro; IPR00975; Interleukin_1.
DR	Pfam; PF00340; IL1_1.
DR	Pfam; PF02394; IL1_propep_1.
DR	ProDom; PD002536; Interleukin_1.
DR	SMART; SM00125; IL1_1.
DR	PROSITE; PS00253; INTERLEUKIN_1.1.
FT	CHAIN 106 267 INTERLEUKIN-1BETA.
SQ	SEQUENCE 267 AA; 29822 MW; 3EF72164B4D40B64 CRC64;
Query Match	14.4%; Score 152.5; DB 13; Length 267;
Best Local Similarity	28.5%; Pred. No. 4.3e-07;
Matches	59; Conservative 31; Mismatches 74; Indels 43; Gaps 11;
QY	2 SALLILALV-----GAAVADYKDDDKLA-----ANSALCRGKVNLNPKK 44
Db	59 AAVLVAMTKLRAPRRSRDFADSD--LSALLEVFEPYFQRLSSYAGAPAFRTSOS 116
QY	45 FSIHDOHKVLVLD-SGNLIV-----PDKNITPELPFALLASSLSAAKGS----- 92
Db	117 FDIPDIHQCFEVLSPQLVALHIGQSSSQKRLNT-----ALYRPGRGSGAGTCQM 170
QY	93 PILGVSKGEFCYCDKDQSGHSPLDLCKELMKLAQGKSARAPFIIFYR--AQVGSMN 150
Db	171 PVALGI-KG-YKLVMSCWMSSTEPTQLLEADVNRKIDSVLTR--PIFYLDPSPTBSTT 226
QY	151 MLESAAHPGWEIFCTSCNCNEBPVGYTD 177
Db	227 RFESAAPFGWFICTSLQPRQVGITNQ 253
RESULT 4	
Q9BEHO	PRELIMINARY; PRT; 176 AA.
AC	O9BEHO:
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE	Interleukin-1 receptor antagonist.
OS	Canis familiaris (dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Plissipedia; Canidae; Canis.
OX	NCBI_TaxID=9615;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Shin I.-S., Youn H.-Y.;
RT	"Molecular cloning of canine interleukin-1 receptor antagonist (IL-
RL	Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AY026462; AAK01472.1; '-'
DR	HSSP; PI8510; IILR
DR	GO; GO:0005576; C:extracellular; IEA
DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA
DR	GO; GO:0004872; F:receptor activity; IEA
DR	GO; GO:0006955; P:immune response; IEA


```
DR InterPro; IPR008996; CytoC IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Receptor.
SQ SEQUENCE 176 AA; 19922 MW; 8486CA54A240212B CRC64;

Query Match 14.3%; Score 151; DB 6; Length 176;
Best Local Similarity 28.9%; Pred. No. 3.6e-07;
Matches 46; Conservative 27; Mismatches 76; Indels 10; Gaps 6;

QY 32 CRGPKVNLNPKKPSIHQDHKVLVDSGNLIAVPDKNYIRPEIFPFLAASSLSASAKG 91
DB 25 CRPIGKAPCRMQARIMDVNOKTYLRNNQLVA---GYLQGS-NTKLEKLDVVPVEPH 79
QY 92 SPILLGVSKGEFCLYCDKQSHPSIQLKKEKLMKLAQKESARRPIFYRAQVGSWM 151
DB 80 A-VFLGHGKCLCLACVKSDETR--LQLEAVNITDLSKNDQDKR-FTFILSDSGPTTS 135
QY 152 LESAAHPGWFICTSCNCPNPVGTDKFENRKH- EFSFQ 189
DB 136 FESAACPGEWFLCTALADRPVSLNRPDEAMVTYKFYQ 174

RESULT 5
Q9GMZ4 PRELIMINARY; PRT; 177 AA.
ID Q9GMZ4
AC Q9GMZ4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-1 receptor antagonist.
GN IL-1RA.
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Tursiops.
OC NCBI_TaxID=9739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2109087; PubMed=11182153;
RA Inoue Y., Icon T., Jimbo T., Syouji Y., Ueda K., Sakai T.;
RT "Molecular cloning and functional expression of bottle-nosed dolphin
RT (Tursiops truncatus) Interleukin-1 receptor antagonist."
RL Vet. Immunol. Immunopathol. 78:131-141(2001).
DR EMBL; AB038268; BAB1806.1; -.
DR HSSP; P18510; 1IRA.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:Interleukin-1 receptor binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; CytoC IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Receptor.
SQ SEQUENCE 177 AA; 19923 MW; 6FD19A06C09B131B CRC64;

Query Match 14.2%; Score 150; DB 6; Length 177;
Best Local Similarity 28.4%; Pred. No. 4.6e-07;
Matches 46; Conservative 21; Mismatches 53; Indels 42; Gaps 6;

QY 45 FSIHDOHKVLVDSGNLIA-----VPDKNYIRPEIFPFLAASSLSASAKG 88
DB 38 FRIDVQKTFYLRNNQVLVAGYLOGPNTKLEKIDVVP---IEPHMF----- 82
QY 89 EKSPILLGVSKGEFCLYCDKQSHPSIQLKKEKLMKLAQKESARRPIFYRAQVGS 148
DB 83 -----LGHGGKCLCLACVKSDEI--KGLERVNTDLSKNDQDKR-FAFIRSDSGP 132
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QY 149 MNLESAHPGWFICTSCNCPNPVGTDKFENRKH- EFSFQ 189
DB 133 TTSFESAACPGEWFLCTALADRPVSLNRPDEAMVTYKFYQ 174

RESULT 6
Q9DDF2 PRELIMINARY; PRT; 272 AA.
ID Q9DDF2
AC Q9DDF2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 1 beta 2-2.
GN IL-1 BETA 2.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Cyprinus.
OC NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Engelma M.Y., Stet R.J.M., Verbarg-van Kemenade L.B.M.;
RT "Cloning and sequencing of two carp interleukin 1 beta 2 complementary
RT DNAs."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ401031; CACI9888.1; -.
DR HSSP; P01584; 211B.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:Interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR008996; CytoC IL1 like.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Receptor.
SQ SEQUENCE 272 AA; 30547 MW; C87FE9D7B6438BE4 CRC64;

Query Match 14.0%; Score 148.5; DB 13; Length 272;
Best Local Similarity 26.2%; Pred. No. 1.1e-06;
Matches 43; Conservative 30; Mismatches 66; Indels 25; Gaps 5;

QY 30 ALCRGPKVNLNPKKPSIHQDHKVLVDSGNLIAVPDKNYIRPEIFPFLAASSLSASAE 89
DB 120 SVCDKRYKKTIVQSKVLNODLHLKAVTLASGT-----IQYKQFPMWTVYSSAQON 170
QY 90 KGSPIILGVSKGEFCLYCDKQSHPSIQLKKEK--LMKLAQKESARRPIFYRAQV 147
DB 171 NGQPVCCGISNSMLYIACIQ-SGSSPVLLLKKEVSGGLNITADDPNGYDLSLFFRKETG 229
QY 148 -SNMLESAAHPGWFICTSCNCPNPVGTDKFENRKHIEFSFQ 190
DB 230 TAVTFESVKYPGWFLSTA-----FDWKKVENSQVP 261

RESULT 7
Q866R8 PRELIMINARY; PRT; 177 AA.
ID Q866R8
AC Q866R8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IL-1 receptor antagonist.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
```

RX MEDLINE=22419343; PubMed=12530978;
 RA Smith D.E., Hanna R., Friend D., Moore H., Chen H., Farese A.M.,
 RA Macvettie T.J., Vitera G.D., Sims J.E.,
 RT "The Soluble Form of IL-1 Receptor Accessory Protein Enhances the
 RT Ability of Soluble Type II IL-1 Receptor to Inhibit IL-1 Action."
 RL Immunity 18:87-96(2003).
 DR EMBL; AY182232; AAC24703.1; "-
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008996; Cytok_IL1_Like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 DR
 QM Receptor. 177 AA; 19892 MW; FB7939A968EF360F CXC64;
 QM SEQUENCE

Query Match	14.0%	Score 148;	DB 6;	Length 177;
Best Local Similarity	30.2%	Pred. No. 7.4e-07;		
Matches	42;	Conservative	26;	Mismatches 57;
			Indels	14;
			Gaps	7;
Qy	42	PKK---PSIHODHVLVDSGNLIAVDPKYYIR-PEIFPALASSLSASAEGSPILLG	97	
Db	32	PSKQAPRIWVNOKTFILRNQQLVA----GLGSPNV--NLEEKIDVPIEPHA-LTLG	84	
Qy	98	VSKGEFLCYCDKDGQSHPSLQLKKEKLMKLAOKESARRPFIYRAOVGSMMNLESAAH	157	
Db	85	IHGKMKICISVSGDETR--LQLEAVNITDLSKNRKQKR--FAFVRSDSGPTTSPESAAC	141	
Qy	158	PGWFICTSCNENEPYGVTD	176	
Db	142	PGWFICTAMEADQPVSLTN	160	

RESULT 9			
ID	OBAXV9	PRELIMINARY;	PRT; 272 AA.
AC	OBAXV9;		
DT	01-MAR-2003 (TREMBLrel. 23, Created)		
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Interleukin-1 beta-1.		
GN	IL-1B-1.		
OS	Carassius auratus (Goldfish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;		
OC	Cyprinidae; Carassius.		
OX	NCBI_TaxID=7957;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RA	Mang T., Bird S., Zou J., Secombes C.J.;		
RT	"Sequencing, gene organisation and differential expression of two		
RT	goldfish IL-1 beta genes";		
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.		
EMBL	AF419848; CAD12102.1; "		
DR	GO; GO:0005576; Cextracellular; IEA.		
DR	GO; GO:0005149; P.interleukin-1 receptor binding; IEA.		
DR	GO; GO:0006855; P.immune response; IEA.		
DR	GO; GO:0006854; P.inflammatory response; IEA.		
DR	InterPro; IPR008996; Cytok_IL1_like.		
DR	InterPro; IPR003502; IL1_propep.		
DR	InterPro; IPR000975; Interleukin_1.		
DR	Pfam; PF00340; IL1; 1.		
DR	Pfam; PF02394; IL1_propep; 1.		
DR	SMART; SM00125; IL1; 1.		
DR	SMART; PS00253; INTERLEUKIN_1; 1.		
DR	SEQUENCE 272 AA; 30721 MW; A91E5D728770E13 CRC64;		

Query Match 13.7%; Score 145.5; DB 13; Length 272;

Best Local Similarity	27.4%	Pred. No. 2.3e+06	
Matches	43	Conservative	31
		Mismatches	66
		Indels	17
		Gaps	5

Qy	31	LCRPPKXKLNPKKFSIHDDHKLVLDSCGLIIVPDKNYIRPELFFLAASLSASAKK	90
	:		
Db	121	ICDXYKKTIVQSNLTINNEEDHLTKAVTTLASAGN-----IQYKRFEMSTYLSAPQNK	171
	:		
Qy	91	GSPIILGVSKGEFLCYCDKDGQSHPSIQLEKKK--IMKLAQKESASAPRPIFYRAQVG-	147
	:		
Db	172	GQFVCLAINSNLTIVACTESDGS--PILIKVEGSLPMTIKVQNGDGLLFFPKETGT	230
	:		
Qy	148	SMNMLGSAHNGWPICTSCNCEVGV---TDKFFEN	180
	:		
Db	231	AYNFFESVKYPGWYISTAFDDMEREMIQVETDRTIN	267
	:		

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RESULT 9
09GKK2
ID 09GKK2 PRELIMINARY; PRT; 176 AA.
AC 09GKK2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Interleukin-1 receptor antagonist.
OS Canis familiaris (Dog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21090992; PubMed=1182158;
RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duchie S.,
RA Bennett D.;
RT "Cloning of canine IL-1ra, TNFR and TIMP-2."
RL Vet. Immunol. Immunopathol. 78:207-214 (2001).
DR EMBL; AF216526; AAC36777.1; -.
DR HSSP; P18510; IILR.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002535; Interleukin_1; 1.
DR SMART; SMO0125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Receptor.
RW SEQUENCE 176 AA; 19938 MW; 8486CA54A254206B CRC64;

```

Query Match	13.3%	Score 141,	DB 6,	Length 176;
Best Local Similarity	28.3%;	Pred. No. 3.7e-06;		
Matches	45;	Conservative	27;	Mismatches 77;
			Indels	10;
			Gaps	6

Qy 32 CRGRKVNKNLPKRSKSHSDQHKKVLVLDSGNLIAPDKNYINPELIFALASSISSASAEKG 91

Db 25 CRPLGRKPCRMQAFRRIDVNDQKTFYLRNNQVLA---GYLQGS-NTKLEBKLDVVPVEPH 79

Qy 92 SPILLGVSKGBFCLYCKDKKGQSHPSIQLKKEKLMKLAQKESARPFIFRAQVGSNM 151

Db 80 A-VELGIGHGGLKLCIACVYSGDETR--LQLEAVNITDLSKNKDQDKR-FTFILLSDSGPTTS 135

Qy 152 LESAAHPGMFICTSCNCCNEPVGIVLDKFEENRCHI--EFSFQ 189

Db 136 FESAAICPMFLCTALAEADRLVSLNRRPEAMVTKFYFQ 174

RESULT 10	
Q9DDF3	
ID Q9DDF3	PRELIMINARY;
AC Q9DDF3	PRT; 272 AA.
DT 01-MAR-2001	(TREMBlrel. 16, Created)
DT 01-MAR-2001	(TREMBlrel. 16, Last sequence update)

	Query Match	Similarity	13.0%	Score	137.5;	DB	13;	Length	272;
	Best Local	Similarity	25.8%	Pred.	No. 1.5e-05;				
	Matches	Conservative	42;	Mismatches	67;	Indels	25;	Gaps	5
QY	31	LGRGPKVKNLPPKKEISHDQHVKLVLDSGNLIAPVDKNYIRPEIFALASSLSASAER	90						
Db	121	VCDKKTKTLVGNSNKLTNQDLHKAVTLLSAGT-----IYKVGFMSPVSSDDPDND	171						
QY	91	GSPILLGVSKBEFCICYCDKDGQSHPISIQLKKE--LMKLAQKESARRPFIFFYAQQVS	148						
Db	172	GQPVLCTGISNSNLVIYACTQ--SGGSPPVLLLKEVSGPLWTITGDGPNGYDSLTFPRKETGT	230						
QY	149	--MNNLESAAHBGMFICTSCNCNEPVGIVDKENRGHIEFSPOP	190						
Db	231	DYNTPESVKYIPGMVFISTA-----FDMDKRVESQVP	261						

Query Match	12.8%	Score 136;	DB 13;	Length 273;
Best Local Similarity	30.7%;	Pred. No. 2.1e-05;		
Matches 50;	Conservative 27;	Mismatches 70;	Indels 16;	Gaps 7;
38 KNLPKKSINDQHKKVLVDSG--NLAVDPKNTIRP-----ELFFALASLS-SASAE 89				

RESULT	12		
057398			
ID	057398	PRELIMINARY;	PRT; 276 AA.
AC	057398;		
DT	01-JUN-1998 (TREMBLrel. 06, Created)		
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Interleukin-1 beta.		
OS	Cyprinus carpio (Common carp).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Cyprinus.		
OX	NCBI_TaxId=7962;		
RN	[1]		
RP	SEQUENCE FROM N.A.		

RT	"Molecular cloning and expression analysis of carp (<i>Cyprinus carpio</i>) interleukin-1beta, high affinity immunoglobulin E Fc receptor gamma subunit and serum amyloid A."
RT	Fish and Shellfish Immunol. 10:1229-242(2000).
RL	EMBL, AB010701, EAA24538.1, --
DR	HSSP, P01584, IHTB.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	GO; GO:0006954; P:inflammatory response; IEA.
DR	InterPro; IPR008936; Cytok IL1 like.
DR	InterPro; IPR003502; IL1 proped.
DR	InterPro; IPR000975; Interleukin_1.
DR	Pfam; PF00340; IL1_1.
DR	Pfam; PF02394; IL1_proped; 1.
DR	SMART; SM00125; IL1_1.
DR	PROSITE; PS00253; INTERLEUKIN_1; 1.
SC	SEQUENCE 276 AA; 31070 MW; F3ACG5BOA3JFD07B3 CRC64;

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Query Match 12.2% / Score 129.5 / DB 13 / Length 276;
Best Local Similarity 23.2% / Pred. No. 9, 7e-05;
Matches 38; Conservative 34; Mismatches 69; Indels 23; Gaps 4

QY   31 LCRGRVKNLNPKEKSIHQDHKVLVDGSLNIAVPDKNYIRREIFFALASSLSAASK 90
Db    123 ICDKKTKMTVGSKNDSDPEHLHKAVTLISAGAM-----QKVGFMSSTFVSASTQKE 173

QY   91 GSPILGVSGKEFCLYCDKDQGSHPSLTOKKEKLMLAAQESARRPFFIYAQGS-W 149
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    174 AQPVLGLGISNSNLTYACTQLDGS--PVLLIKESAQSGVNITIKADPNDSLIFPKKETRY 232

QY   150 NMLESAHPGWICTSCNENEPVGTDRKENKHIEFSQPCK 193
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db    233 NTFESEVKTPGMFLSTA-----PDDEKEEMNNOMPTTR 264

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RESULT	13	
Q9PM18		
Q9PM18	PRELIMINARY;	PRT: 276 AA.
AC	Q9PM18	
DT	01-MAY-2000	(REMBLrel. 13, Created)
DT	01-MAY-2000	(REMBLrel. 13, Last sequence update)
DT	01-OCT-2003	(REMBLrel. 25, Last annotation update)
DE	Interleukin-1-beta.	

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GN IL-1.
OS Cypripus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxId=7962;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21098506; Pubmed=1164885;
RA Engelisma M.Y., Steet R.J.M., Schipper H., Verburg-van Kemenade B.M.L.;
RT "Regulation of interleukin 1 beta RNA expression in the common carp,
RT Cypripus carpio L." 25:195-203 (2001).
RL Dev. Comp. Immunol. 25:195-203 (2001).
DR HSSP; P01584; IHB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR003502; IL1_propep.
DR Pfam; PF00340; IL1_1.
DR Pfam; PF02394; IL1_propep; 1.
DR SMART; SM00125; IL1_1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ SEQUENCE 276 AA; 31098 MW; 4AE31E2564A97C6A CRC64;

Query Match 12.1%; Score 129.5; DB 13; Length 276;
Best Local Similarity 23.2%; Pred. No. 9.7e-05;
Matches 38; Conservative 34; Mismatches 69; Indels 23; Gaps 4;

QY 31 LCRGPKVKNLNPCKFSIHDDHKLVLVDSGNLJAVFDKNYRPEIFPALASLSASAER 90
DB 123 ICRKTKTWQSVKSLDDEPHLAKVILISAAM-----QYKQFSMTFYSATQKE 173
QY 91 GSDPILGVSKGEFCYCDKDGQSHPSLQKKEKMKLAQKESARRPFIYRAQVGS-W 149
DB 174 AQVCCIGISNSNLYLACTQDGS-PVLILKEASGVNTIKADPDNSLFFPKETGTRY 232
QY 150 NMLESAHPGWFCTSCNCEPEYGVTDKFNKRKHIESFPQVK 193
DB 233 NTFESVYKPGWFISTA-----FDMWEKVENQMPTR 264

RESULT 14
ID 08AXV8 PRELIMINARY; PRT; 238 AA.
AC 08AXV8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-1 beta-2.
GN IL-1B-2.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxId=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Wang T., Bird S., Zou J., Secombes C.T.;
RT "Sequencing, gene organisation and differential expression of two
RT goldfish IL-1 beta genes." 1;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ419849; CAD12103.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR003502; IL1_propep.

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DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1_1.
DR Pfam; PF02394; IL1_propep; 1.
DR SMART; SM00125; IL1_1.
SQ SEQUENCE 238 AA; 27076 MW; 71BCC1719B7DFB07 CRC64;

Query Match 12.1%; Score 128.5; DB 13; Length 238;
Best Local Similarity 24.8%; Pred. No. 0.0001;
Matches 35; Conservative 31; Mismatches 50; Indels 25; Gaps 5;

QY 53 KYLVLDGSLVDPDKNYRPEIFPALASLSASAERKSPILLGVSKGEFCYCDKDG 112
DB 103 KAVTISAGTM-----QYKQFSMTFYSATQKQAPVCLISNSNLYLACTQSDG 153
QY 113 OSHPSLQKKEK-LMKLAQKESARRPFIYRAQVGS-SMNMLESAHPGWFCTSCN 169
DB 154 SS-PALILKEVVGPLNTITRDDPNGNDLSLFFPKETGTAYNFESVYKPGWFIITTA----- 208
QY 170 EPVGVTDKFNKRKHIESFPQ 190
DB 209 -----FDMWEKVENQMP 221

RESULT 15
ID 029082 PRELIMINARY; PRT; 267 AA.
AC 029082;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 1-beta.
GN INTERLEUKIN 1-BETA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Vanderbroeck K.;
RT Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94039070; Pubmed=8223584;
RA Vanderbroeck K., Fiten P., Beuken E., Martens E., Janssen A.,
RT "Gene sequence, cDNA construction, expression in Escherichia coli and
RT genetically approached purification of porcine interleukin-1beta." 1;
RL Eur. J. Biochem. 217:45-52 (1993).
DR EMBL; X74568; CAA52660.1; -.
DR PIR; S38373; S38373.
DR HSSP; P01584; IHB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1_1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1_1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ SEQUENCE 267 AA; 29893 MW; 4830645DA5FF9967 CRC64;

Query Match 12.1%; Score 128; DB 6; Length 267;
Best Local Similarity 28.9%; Pred. No. 0.00013;
Matches 43; Conservative 28; Mismatches 66; Indels 12; Gaps 6;

```

QY	27	ANSALCRGPKVKNLNPKEFSIHODHKVVLDSGNLAVPD-KNYIRPEIFPALASSLS	84
Db	107	ANGFLCDATPVQSVDC--LQDKDEKALVLAGPHELKALHLKQDLKREVVFCMSFYQG	163
QY	85	SASAEKSPILLGVSKGEFCLYC-DKDXGSHPSIQLKKEKMLAQAQESARRPFIYR	143
Db	164	DDSDDK-IPVTLGIGKKNLYLSCVWKD--DTPTLQ--EDVDPKSYPKRDMERFVYK	217
QY	144	AQVGSMMNLESAHPGWFICTSCNCEPV	172
Db	218	TEIKNRVFEBSALYPNNYISTQAQKPV	246

Search completed: September 9, 2004, 13:27:43
 Job time : 120 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:12:44 ; Search time 23 Seconds
(without alignments)
459.576 Million cell updates/sec

Title: US-09-869-566-5
Perfect score: 1059
Sequence: 1 MSALLILALVCAAVADYKD.....IEFSFQPCAKMSPSEVSD 203

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	895	84.5	218	1 IF7_HUMAN	Q9N2H6 homo sapien
2	229.5	21.7	169	1 IF9_HUMAN	Q9N2H6 homo sapien
3	209	19.7	158	1 IF6_HUMAN	Q9N2H6 homo sapien
4	199	18.8	183	1 IF8_MOUSE	Q9N2H6 homo sapien
5	191.5	18.1	156	1 IF5_MOUSE	Q9N2H6 homo sapien
6	174.5	16.5	155	1 IF5_HUMAN	Q9N2H6 homo sapien
7	174.5	16.5	164	1 IF9_MOUSE	Q9N2H6 homo sapien
8	171	16.1	160	1 IF6_MOUSE	Q9N2H6 homo sapien
9	167	15.8	178	1 IF6_MOUSE	Q9N2H6 homo sapien
10	165.5	15.6	152	1 IF6_MOUSE	Q9N2H6 homo sapien
11	158.5	15.0	177	1 IF6_HUMAN	Q9N2H6 homo sapien
12	156.5	14.8	152	1 IF6_HUMAN	Q9N2H6 homo sapien
13	154.5	14.6	177	1 IF6_HUMAN	Q9N2H6 homo sapien
14	152	14.4	174	1 IF6_HUMAN	Q9N2H6 homo sapien
15	151	14.3	176	1 IF6_HUMAN	Q9N2H6 homo sapien
16	150	14.2	177	1 IF6_HUMAN	Q9N2H6 homo sapien
17	146.5	13.8	177	1 IF6_HUMAN	Q9N2H6 homo sapien
18	146.5	13.8	178	1 IF6_HUMAN	Q9N2H6 homo sapien
19	137.5	13.0	177	1 IF6_HUMAN	Q9N2H6 homo sapien
20	131.5	12.4	266	1 IL1B_MOUSE	Q9N2H6 homo sapien
21	121.5	11.5	267	1 IL1B_MOUSE	Q9N2H6 homo sapien
22	121	11.4	268	1 IL1B_MOUSE	Q9N2H6 homo sapien
23	120.5	11.4	269	1 IL1B_MOUSE	Q9N2H6 homo sapien
24	118.5	11.2	164	1 IL1B_MOUSE	Q9N2H6 homo sapien
25	118	11.1	266	1 IL1B_MOUSE	Q9N2H6 homo sapien
26	113.5	10.7	266	1 IL1B_MOUSE	Q9N2H6 homo sapien
27	105.5	10.0	266	1 IL1B_MOUSE	Q9N2H6 homo sapien
28	101	9.5	268	1 IL1B_MOUSE	Q9N2H6 homo sapien
29	99	9.3	268	1 IL1B_MOUSE	Q9N2H6 homo sapien
30	98.5	9.3	269	1 IL1B_MOUSE	Q9N2H6 homo sapien
31	98	9.3	266	1 IL1B_MOUSE	Q9N2H6 homo sapien
32	95.5	9.0	246	1 TRY2_MOUSE	Q9N2H6 homo sapien
33	92.5	8.7	268	1 IL1B_MOUSE	Q9N2H6 homo sapien

34	91	8.6	404	1 KTR3_YEAST	P38130 saccharomyc
35	89.5	8.5	267	1 IL1B_MOUSE	P41687 felis silve
36	89	8.4	269	1 IL1B_MOUSE	P51493 macaca neme
37	88.5	8.4	269	1 IL1B_MOUSE	P46648 cercopithec
38	88.5	8.4	269	1 IL1B_MOUSE	P46090 macaca mula
39	88	8.3	473	1 MDM2_XENLA	P56273 xenopus lae
40	84	7.9	270	1 IL1A_MOUSE	P79182 macaca fasc
41	83.5	7.9	268	1 IL1B_MOUSE	P00762 rattus norv
42	82.5	7.8	246	1 TRY1_RAT	Q9N2H6 homo sapien
43	81	7.6	320	1 MOA1_MOUSE	Q9N2H6 homo sapien
44	81	7.6	1058	1 U202_ARATH	Q9N2H6 homo sapien
45	80.5	7.6	246	1 TRY2_RAT	P00763 rattus norv

ALIGNMENTS

RESULT 1	ID	IF7_HUMAN	STANDARD	PRT	218 AA
AC	Q9N2H6	Q9N2H6	Q9N2H6	Q9N2H6	Q9N2H6
DT	28-FEB-2003	Rel. 41, Created			
DT	28-FEB-2003	Rel. 41, Last sequence update			
DT	10-OCT-2003	Rel. 42, Last annotation update			
DE	Interleukin 1 family member 7 precursor (IL-1F7) (Interleukin-1 zeta)				
DE	(IL-1 zeta) (F1L1 zeta) (Interleukin-1 homolog 4) (IL-1H4)				
DE	(Interleukin-1-related protein) (IL-1RP1) (IL-1X protein).				
GN	IL1F7 OR IL1L1Z OR IL1H4 OR IL1RP1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RN	SEQUENCE FROM N.A. (ISOFORM B).				
RC	TISSUE=Fetal B-cell, Fetal colon, Fetal lung, and Fetal testis;				
RC	MEDLINE=20209405; PubMed=10744718;				
RA	Kumar S., McDonnell P.C., Lehr R., Tierney L., Tamas M.N.,				
RA	Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,				
RA	Young P.R.;				
RT	"Identification and initial characterization of four novel members of				
RT	the interleukin-1 family.";				
RL	J. Biol. Chem. 275:10308-10314(2000).				
RN	[2]				
RN	SEQUENCE FROM N.A. (ISOFORM B).				
RC	TISSUE=Colon carcinoma;				
RC	Manoj P.P., Mantovani A., Muzio M.;				
RA	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RN	SEQUENCE FROM N.A. (ISOFORMS B AND C), SEQUENCE OF 46-54, AND VARIANTS				
RC	VAL-31 AND ALA-42.				
RC	MEDLINE=2106552; PubMed=1145836;				
RA	Pan G., Risse P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,				
RA	Yasuda D., Lewis L., Eigenbrodt C., Henzel W.J., Vandlen R.;				
RT	"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-				
RT	1RNP.";				
RL	Cytokine 13:1-7(2001).				
RN	[4]				
RN	SEQUENCE FROM N.A. (ISOFORM A).				
RC	MEDLINE=20092888; PubMed=10625660;				
RA	Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,				
RA	Sims J.E.;				
RT	"Four new members expand the IL-1 superfamily.";				
RL	J. Biol. Chem. 275:11659-1175(2000).				
RN	[5]				
RN	SEQUENCE FROM N.A. (ISOFORMS D AND E).				
RC	MEDLINE=21988051; PubMed=11991723;				
RA	Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;				
RT	"Genomic organization of the interleukin-1 locus.";				
RL	Genomics 79:726-733(2002).				
RN	[6]				
RN	SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS VAL-31 AND ALA-42.				
RC	TISSUE=Placenta;				
RC	MEDLINE=22388257; PubMed=12477932;				

RA Strausberg R.D., Fellings E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKenna K.J., Malek J.A., Gunnarane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs J.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dixon M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield A., Schein J.E., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences".
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Binds to interleukin-18 receptor (IL-18R) receptor but
CC not to IL-1 receptor. Could be a new player in the inflammatory
CC and immune responses mediated by the IL-18/IL-18R axis.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC Event-Alternative splicing; Named isoforms=5;
CC Name=B;
CC IsoId=G9NZH6-1; Sequence=Displayed;
CC Name=A;
CC IsoId=G9NZH6-2; Sequence=VSP_002653;
CC Name=C;
CC IsoId=G9NZH6-3; Sequence=VSP_002656;
CC Name=D;
CC IsoId=G9NZH6-4; Sequence=VSP_002654;
CC Name=E;
CC IsoId=G9NZH6-5; Sequence=VSP_002655;
CC -1- TISSUE SPECIFICITY: Isoforms A, B and C are expressed in testis,
CC colon, placenta, lung and lymph node. Isoforms D and E were found
CC only in testis and bone marrow, whereas only isoform A is found in
CC brain, only isoform B in kidney and only isoform C in heart.
CC -1- INDUCTION: By phorbol ester (PMA) in different cell lines.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC
CC -----
DR EMBL; AF200496; AAF69252.1; -
DR EMBL; AF167368; AAG29344.1; -
DR EMBL; AF251118; AAG14420.1; -
DR EMBL; AF251120; AAG14422.1; -
DR EMBL; AF251119; AAG14421.1; -
DR EMBL; AF201832; AAF25212.1; -
DR EMBL; AY071840; AAL67151.1; -
DR EMBL; AY071841; AAL67154.1; -
DR EMBL; BC020637; AAR20637.1; -
DR HSSP; P18510; IL1R.
DR Genew; HGNC:15563; IL1F7.
DR MIM; 605510; -
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0005149; F:interleukin-1 receptor binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SMO0125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; FALSE NEG.
CW Cytokine; Multisub; Interleukin; Alternative splicing; Polymorphism.

FT	PROBE	1	45	REMOVED IN MATURE FORM.
FT	CHAIN	46	218	INTERLEUKIN 1 FAMILY MEMBER 7.
FT	VARSPLIC	1	49	MSPIFGNSGVGMGSEDMEDKEDPOCCEDBPASSPLERGPSLP
FT				TWNVFVHTS -> MSGCDRRETEYTKGNSFKQRLRG (in
FT				isoform A).
FT	VARSPLIC	28	49	/FtId=VSP_002653.
FT				DPASSPLERGPSLPTMNVFHTS -> G (in isoform
FT				D).
FT	VARSPLIC	28	88	/FtId=VSP_002654.
FT				Missing (in isoform E).
FT	VARSPLIC	49	89	/FtId=VSP_002655.
FT				SPKVNLPNPKFSDHDDHVKVLDLSDGNLIAVPDKNYIRPE
FT				-> K (in isoform C).
FT	VARIANT	31	31	/FtId=VSP_002656.
FT				G -> V.
FT	VARIANT	42	42	/FtId=VAR_014260.
FT				T -> A.
FT	VARIANT	42	42	/FtId=VAR_014261.
FT				/FtId=VAR_014261.
FT	SEQUENCE	218 AA;	24126 MM;	96BE08931DD2C6A68 CRC64;
FT				
FT	Query Match	84.5%;	Score 895;	DB 1;
FT	Best Local Similarity	100.0%;	Pred. NO. 1.3e-77;	
FT	Matches 169;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY		35	PKVKNLNKKRSHDQHKVYLDLSDGNLIAVPDKNYIRPEIFPPLASSLSASAERKSPGI	94
DB		50	PKVKNLNKKRSHDQHKVYLDLSDGNLIAVPDKNYIRPEIFPPLASSLSASAERKSPGI	109
QY		95	LLGVSGKGFCLCYCDKDKQSHPSIQLKKKKMLKLAQKESARRPEIFPRAQVGSNNMLES	154
DB		110	LLGVSGKGFCLCYCDKDKQSHPSIQLKKKKMLKLAQKESARRPEIFPRAQVGSNNMLES	169
QY		155	AAHPGWFICTSCNCNEPVGVTDKFENRKHIFFSFQPVCKAEMSPREVS	203
DB		170	AAHPGWFICTSCNCNEPVGVTDKFENRKHIFFSFQPVCKAEMSPREVS	218
RESULT 2				
11F9_HUMAN	STANDARD;	PRT;	169 AA.	
AC	O9NZH8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Interleukin 1 family member 9 (IL-1F9) (Interleukin-1 homolog 1) (IL-1H1) (Interleukin-1 epsilon) (IL-1 epsilon) (IL-1 related protein 2) (IL-1RP2).			
DE	IL1F9 OR IL1H1 OR IL1E OR IL1RP2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISUB=Keratinoctes;			
RX	MEDLINE=20209405; PubMed=10744718;			
RA	Kumar S., McConnell P.C., Lehr R., Tierney L., Tzimas M.N.,			
RA	Grissold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,			
RA	Young P.R.;			
RT	"Identification and initial characterization of four novel members of			
RT	the interleukin-1 family."			
RL	J. Biol. Chem. 275:10308-10314 (2000).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	TISUB=Epithelium;			
RX	MEDLINE=2135532; PubMed=1466363;			
RA	Debets R., Tlmanis U.C., Homey B., Zurawski S., Sana T.R., Lo S.,			
RA	Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,			
RA	Kastelein R.A.;			
RT	"Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function			
RT	as an antagonist and agonist of NF-kappa B activation through the			
RT	orphan IL-1 receptor-related protein 2."			
RL	J. Immunol. 167:1440-1446 (2001).			


```

RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20318623; PubMed=10860666;
RA Bufield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
RT "Identification and gene organization of three novel members of the
RT IL-1 family on human chromosome 2.";
RL Genomics 66:213-216(2000).
CC
CC -1- FUNCTION: Function as an agonist of NF-kappa B activation through
CC the orphan IL-1-receptor-related protein 2. Could constitute part
CC of an independent signaling system analogous to interleukin-1
CC alpha (IL-1a), beta (IL-1b) receptor agonist and interleukin-1
CC receptor type 1 (IL-1R1), that is present in epithelial barriers
CC and takes part in local inflammatory response.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Highly expressed in tissues containing
CC epithelial cells: skin, lung, stomach and esophagus. In skin is
CC expressed only in keratinocytes but not in fibroblasts,
CC endothelial cells or melanocytes. Up-regulated in lesional
CC psoriasis skin.
CC -1- INDUCTION: By TNF-alpha and by IFN-gamma in keratinocytes.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC -----
DR EMBL: AF200492; AAF69248.1; -
DR EMBL: AF206696; AAG35670.1; -
DR HSSP: P18510; IL1F6.
DR Genew: HGNC:15741; IL1F9.
DR MIM: 605542; -
DR GO: GO:0007267; P:cell-cell signaling; TAS.
DR GO: GO:0009613; P:response to pest/pathogen/parasite; TAS.
DR InterPro: IPR008996; CytoK_IL1like.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; FALSE_NEG.
DR CytoKine; MultiGene family.
KW SEQUENCE 169 AA; 18721 MW; F00A9243706FA154 CRC64;
SQ
Query Match 31.7%; Score 229.5; DB 1; Length 169;
Best Local Similarity 35.0%; Pred. No. 1.2e-14;
Matches 56; Conservative 29; Mismatches 62; Indels 13; Gaps 5;
QY 19 DDDDKLAANASALCRGPKVKNLNFKEFSIHDDQHKVLVLDGSLIAYDPKNYIRPEIFFA 78
DB 7 DADGGRVAVQSMK-----PITGINDLNQOQWTLGQNLVAVDRSSVTPVAV 58
QY 79 LASSLSASAE-KSPILIVSKGEFLCYDXKQSHPSIQLKKEKIMKLAQKESARR 137
DB 59 ITCKYPALRGGRDPIYLGIGNPEMCLYCEKVEQ--PTLQLEKQIMDLVYGPPEV-K 115
QY 138 PFIFYRAOVGSMMLESAAHPGFICTSCNCPNEPVGTDK 177
DB 116 PFLFYRAKTGRTSLTESVAFPPDWFIASS-KRDPIILTSE 154

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GN IL1F6 OR IL1E OR F1L1E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBT_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Kenschaw B.R., Ketchum R.R., Kudin M., Garika K.E.,
RA Sims J.E.;
RT "Four new members expand the IL-1 superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in immune system and fetal brain,
CC but not in other tissues tested or in multiple hematopoietic cell
CC lines.
CC -1- MISCELLANEOUS: Binding analysis failed to detect interaction with
CC multiple IL1R family members.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF201831; AAF25211.1; -
DR HSSP: P18510; IL1R.
DR Genew: HGNC:15562; IL1F6.
DR MIM: 605509; -
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0005149; F:interleukin-1 receptor binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR008996; CytoK_IL1like.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; FALSE_NEG.
DR CytoKine; MultiGene family.
KW SEQUENCE 158 AA; 17684 MW; 469AC84306BDE280 CRC64;
SQ
Query Match 19.7%; Score 209; DB 1; Length 158;
Best Local Similarity 36.7%; Pred. No. 9.3e-13;
Matches 54; Conservative 26; Mismatches 61; Indels 6; Gaps 4;
QY 42 PKKFSIHDDQHKVLVLDGSLIAYDPKNYIRPEIFFLAS--SLSSASAEKGSPIILGV 99
DB 10 PQGGSIQIDINHRVWVLODQTLIAPRRDRMSF-VTALISCRHETLEKRGNGIYIGLN 68
QY 100 KGEFLCYDDKQSGSHPSIQLKKEKIMKLAQKESARPFIFYRAOVGSMMLESAAHPG 159
DB 69 GNLICLMCAVGDQ--PTLQLEKQIMDLVYGPPEV-KSLFLFHSQSGRSTFSSVAFPG 125
QY 160 WFICTSCNCPNEPVGTDKFNRRHIEF 186
DB 126 WFIIVSSEGGCPILITQELGKANTTDF 152

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RESULT 3
ID IL1F6 HUMAN STANDARD; PRT; 158 AA.
AC OSURAT;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Interleukin 1 family member 6 (IL-1F6) (Interleukin-1 epsilon) (IL-
DE 1 epsilon) (F1L1 epsilon).

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RESULT 4
ID IL1F8 MOUSE STANDARD; PRT; 183 AA.
AC OSD6Z6; OSR461;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin 1 family member 8 (IL-1F8).
GN IL1F8 OR F1L1E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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CC -1- TISSUE SPECIFICITY: Highly abundant in embryonic tissue and
CC tissues containing epithelial cells.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC or send an email to license@emb-stb.ch).
CC -----
DR EMBL; AF230378; AAF91275.1; -
DR EMBL; AK009741; BAB26471.1; -
DR EMBL; AK008977; BAB26002.1; -
DR EMBL; AJ250429; CAB59831.1; ALT_INIT.
DR EMBL; AF200495; AAF69251.1; -
DR HSSP; P18510; IL1R.
DR MGD; MGI:1859325; IL1F5.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR00975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD02536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Cytokine; Multigene family.
KW CONFLICT 2
FT SEQUENCE 156 AA; 1736 MW; AADIE2F93CF7A7 CFC64;
SQ
Query Match 18.1%; Score 191.5; DB 1; Length 156;
Best Local Similarity 35.1%; Pred. No. 4.2e-11;
Matches 53; Conservative 24; Mismatches 51; Indels 23; Gaps 6;
QY 28 NSALCRGPKVKNLNPKEFSIHDOHKVLVDLSGNIIA--VPDKNYIREPIFALASSISS 85
DB 5 SGALC-----FRMKDSALKVLYLNNOQLAGLHAKEVIKGEISIVPNRALD 52
QY 86 ASAKGSPILILGVKGEFCLCDKDKGSHSLQKKEKMKL-AAQKESARRPIFPRA 144
DB 53 ASL---SPVILVGVGGSGQLSCGTEKG---FLIKLEPVNIMELYGAKES--KSFIFYRR 104
QY 145 QVGSNMNLESAHPGPFICTSCNCPNPGVVT 175
DB 105 DMGLTSSFEAAYPGWFICTSPADQPVRLT 135
RESULT 6
11F5_HUMAN
ID_11F5_HUMAN STANDARD; PRT; 155 AA.
AC QGUBHO;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin 1 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1
DE delta) (FLLI delta) (Interleukin-1-like protein 1) (IL-1L1)
DE (Interleukin-1 H1) (IL-1H1) (Interleukin-1 receptor antagonist
DE homolog 1) (IL-1ra homolog 1) (IL-1 related protein 3) (IL-1RP3).
GN IL1F5 OR FILD OR IL1H1 OR IL1L1 OR IL1RP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
RA Smeets J.E.,
RT "Four new members expand the IL-1 superfamily.";
RL J. Biol. Chem. 275:1169-1175 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=fetal skin;

RX MEDLINE=99443727; PubMed=10512743;
RA Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
RA Dmanac R., Ford J.B.,
RT "IL1H1: a novel interleukin-1 receptor antagonist gene.";
RL Biochem. Biophys. Res. Commun. 263:702-706 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20545217; PubMed=11093146;
RA Barton J.V., Herbst R., Bosisto D., Higgins L., Nicklin M.J.H.,
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
RL Eur. J. Immunol. 30:3299-3308 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359532; PubMed=11466363;
RA Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
RA Kastelen R.A.,
RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
RT as an antagonist and agonist of NF-kappa B activation through the
RT orphan IL-1 receptor-related protein 2.";
RL J. Immunol. 167:1440-1446 (2001).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20318623; PubMed=10860666;
RA Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
RA Zhou H., Leidy K.R., Holmgren L.M., Geating D.P., Pan Y.,
RT "Identification and gene organization of three novel members of the
RT IL-1 family on human chromosome 2.";
RL Genomics 66:213-216 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Aleschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Is a highly and a specific antagonist of the IL-1
CC receptor-related protein 2-mediated response to interleukin 1
CC family member 9 (IL1F9). Could constitute part of an independent
CC signaling system analogous to interleukin-1 alpha (IL-1A), beta
CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
CC 1R1) that is present in epithelial barriers and takes part in
CC local inflammatory response.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in keratinocytes but
CC not in fibroblasts, endothelial cells or melanocytes. Detected
CC also in the spleen, brain leukocyte and macrophage cell types.
CC Increased in lesional psoriasis skin.
CC -1- INDUCTION: By photol ester (PMA) and lipopolysaccharide (LPS)
CC treatment in macrophage cell line.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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DR EMBL; AF201830; AAF25210.1; -
 DR EMBL; AF186094; AAF02757.1; -
 DR EMBL; AJ242737; CAB59823.1; -
 DR EMBL; AJ242738; CAB59823.1; -
 DR EMBL; AJ271338; CAB67704.1; -
 DR EMBL; AF216693; AAF76981.1; -
 DR EMBL; AF230377; AAF91274.1; -
 DR EMBL; BC024747; AAF24747.1; -
 DR PIR; JCT104; JCT104.
 DR HSSP; P18510; IILF.
 DR Genew; HSCN;15561; IILF5.
 DR MIM; 605507; -
 DR GO; GO:0005152; F:Interleukin-1 receptor antagonist activity; TAS.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 DR Cytokine; Multigene family.
 KM SEQUENCE 155 AA; 16962 MW; B96DB5EFA2612E25 CRC64;
 SQ

Query Match 16.5%; Score 174.5; DB 1; Length 155;
 Best Local Similarity 32.0%; Pred. No. 1,7e-09;
 Matches 54; Conservative 18; Mismatches 48; Indels 49; Gaps 7;

QY 28 NSALCRGPVKYNLPKKEFHHDDHKVLDVDSGNLAVPDKNYIRPEIFPALASSISAS 87
 DB 4 SGALC-----FRKDSALKVLYHNNQ-----LAGGLHAGK 35

QY 88 AEKG-----SPILGVSKGEFCLYCDKQSGHPSIQKKEKMLK-AQ 131
 DB 36 VINGEETSVVPRNMLDASLPVILGVGGSGCLSC--GVGQ-EPTLTLERVINIMELYGA 92

QY 132 KESARRPFTYRAOVGSMMNLESAHFGVFTCTSCNCEPVGVTDKREN 180
 DB 93 KES--KSFTEYRRDMGLTSSFSMAAYGPWPLCTVPEADQVRLTQAPEN 139

RESULT 7
 IIF9_MOUSE STANDARD; PRT; 164 AA.
 ID IIF9_MOUSE
 AC Q8R460;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin 1 family member 9 (IL-1F9).
 GN IL1F9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=21988051; Pubmed=11991723;
 RA Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
 RT "Genomic Organization of the interleukin-1 locus.";
 RL Genomics 79:726-733(2002).
 CC -1- FUNCTION: Function as an agonist of NF-kappa B activation through
 CC the orphan IL-1-receptor-related protein 2. Could constitute part
 CC of an independent signaling system analogous to interleukin-1
 CC alpha (IL-1a), beta (IL-1b) receptor agonist and interleukin-1
 CC receptor type 1 (IL-1RI), that is present in epithelial barriers
 CC and takes part in local inflammatory response (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-1 family.

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DR EMBL; AY071843; AAL67153.1; -
 DR MGD; MGI:2449929; I11f9.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
 KM Cytokine; Multigene family.
 SQ SEQUENCE 164 AA; 18733 MW; A7338D475DFEADBE CRC64;
 SQ

Query Match 16.5%; Score 174.5; DB 1; Length 164;
 Best Local Similarity 31.7%; Pred. No. 1,8e-09;
 Matches 45; Conservative 26; Mismatches 66; Indels 5; Gaps 4;

QY 47 HHDQHKVLDVDSGNLAVPDKNYIRPEIFPALASL-SSASAEKSPILLGVSKGEFL 105
 DB 22 VFLLDQQWVIFRQALVTPRSHRVPTVTLPCRYPSRLQDKXIALYLVQNPDKLT 81

QY 106 YCDKDKGSHPSIQKKEKMLKLAQKESARRPFTYRAOVGSMMNLESAHFGVFTCT 165
 DB 82 FCKEVNG--HPTLLKEKILDIYHHP--PKRPLFHYHTRGTSTFESVAAPGHYIASS 138

QY 166 CNCNEPVGVTDKFNKHIIFS 187
 DB 139 KTCN-PIPLTSKKGGEYNNINFN 159

RESULT 8
 IIF6_MOUSE STANDARD; PRT; 160 AA.
 ID IIF6_MOUSE
 AC Q9ULR2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Interleukin 1 family member 6 (IL-1F6) (interleukin-1 epsilon) (IL-1
 epsilon) (F1L1 epsilon) (interleukin-1 homolog 1) (IL-1H1).
 GN IIF6 OR F1L1E OR IL1E OR IL1H1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20209405; Pubmed=10744718;
 RA Kumar S., McDonnell P.C., LeRoy R., Tierney L., Tzimas M.N.,
 RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
 RA Young P.R.;
 RT "Identification and initial characterization of four novel members of
 RT the interleukin-1 family.";
 RL J. Biol. Chem. 275:10308-10314(2000).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21359532; Pubmed=11466363;
 RA Debes R., Timens J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
 RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
 RA Kastelein R.A.;
 RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
 RT as an antagonist and agonist of NF-kappa B activation through the
 RT orphan IL-1 receptor-related protein 2.";
 RL J. Immunol. 167:1440-1446(2001).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;

RA MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavaletto T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Watanabe T.,
 RA Sakai K., Okita T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boileau D., Bolunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernicich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima R., Mazzarelli J., Momberte P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 CC -1- SUBCELLULAR LOCATION: Secreted (potential).
 CC -1- TISSUE SPECIFICITY: Highly expressed in embryonic tissue and in
 CC tissues containing epithelial cells.
 CC -1- MISCELLANEOUS: Binding analysis failed to detect interaction with
 CC multiple IL1R family members.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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 CC -----
 CC EMBL: AF200493; AAF69249.1; -;
 CC EMBL: AF206697; AAG35671.1; -;
 CC EMBL: AK004061; BAB23147.1; -;
 CC HSSP: P01584; 1H1B.
 CC MGD: MGI:1859324; 111f6.
 CC InterPro: IPR008996; Cyclo IL1 like.
 CC InterPro: IPR000975; Interleukin_1.
 CC Pfam: PF00340; IL1; 1.
 CC ProDom: PD002536; Interleukin_1; 1.
 CC SMART: SM00125; IL1; 1.
 CC PROSITE: PS00253; INTERLEUKIN_1; FALSE_NEG.
 CC CycloLine: Multigene family.
 CC KW SEQUENCE 160 AA; 18015 MW; AA0434D68FF62F4A CRC64;
 Query Match 16.1%; Score 171; DB 1; Length 160;
 Best Local Similarity 31.6%; Pred. No. 3.8e-09;
 Matches 43; Conservative 25; Mismatches 62; Indels 6; Gaps 4;
 Oy 36 KVKNLNPKKFSIHDDHKVLVLDGSLAVDPKXNYRREIFPAL-ASSLSASAKSPPI 94
 Db 6 ELRAASPELRHVQDSSRWVLDNNITLAVPKKEGTAVTTTLFCQYLDLTLETNRGPT 65
 Oy 95 LLAGVSGEFCFLCYCDKQSGHPSLQTKKELMKLAQKESARPRPFPAQVGSWMNES 154
 Db 66 YMGVGRPWSCLFCTCTDGGQ--PVLQDGGNIMEMNKKEPKYAS-LFHKXSGTSTRES 122
 Oy 155 AAHPGWF--CTSCNC 168
 Db 123 AAPGWFVAVCSKSGSC 138
 RESULT 9
 IL1X_MOUSE STANDARD; PRT; 178 AA.
 AC P25085; Q70207;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IL-1RN)
 GN (IL1RP).
 GN IL1RN OR IL-1RA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=91250712; PubMed=1828262;
 RA Zahedi K., Seldin M.F., Rits M., Ezeokwiz R.A., Whitehead A.S.;
 RT "Mouse IL-1 receptor antagonist protein. Molecular characterization,
 RT gene mapping, and expression of mRNA in vitro and in vivo.";
 RL J. Immunol. 146:4228-4233(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=91316273; PubMed=1830498;
 RA Matsushima H., Ransel M.F., Matsushima K., Hashinuma A., Sherr C.J.;
 RT "Cloning and expression of murine interleukin-1 receptor antagonist
 RT in macrophages stimulated by colony-stimulating factor 1.";
 RL Blood 78:616-623(1991).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX STRAIN=Swiss;
 RX MEDLINE=94271931; PubMed=8003626;
 RA Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
 RT "The mouse interleukin 1 receptor antagonist protein: gene structure
 RT and regulation in vitro.";
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX STRAIN=FVB X DBA/1 LACJ;
 RX MEDLINE=98209757; PubMed=9550387;
 RA Gabay C., Porter B., Fantuzzi A., Arend W.P.;
 RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning
 RT and protein expression of intracellular isoform and tissue
 RT distribution of secreted and intracellular IL-1 receptor antagonist in
 RT vivo.";
 RL J. Immunol. 159:5905-5913(1997).
 RN [5]
 RP SEQUENCE OF 7-178 FROM N.A.
 RX MEDLINE=91271363; PubMed=1828896;
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
 RA Brandhuber B.J., Thompson R.C.;
 RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
 RT gene family: evolution of a cytokine control mechanism.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
 RN [6]
 RP SEQUENCE OF 23-178 FROM N.A.
 RX MEDLINE=92037824; PubMed=1834470;
 RA Shuck M.E., Bessalu T.E., Tracey D.E., Bienkowski M.J.;
 RT "Cloning, heterologous expression and characterization of murine
 RT interleukin 1 receptor antagonist protein.";
 RL Eur. J. Immunol. 21:2775-2780(1991).
 CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
 CC receptor. Has no IL-1 like activity.
 CC -1- SUBCELLULAR LOCATION: Secreted (isoform 1). Cytoplasmic (isoform
 CC 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P25085-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P25085-2; Sequence=VSP_002652;
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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 CC -----
 DR EMBL; M74294; AAA39309.1; -
 DR EMBL; M64404; AAA39277.1; -
 DR EMBL; L32838; AAA20576.1; -
 DR EMBL; AF001795; AAC15251.1; -
 DR EMBL; M57525; AAA39278.1; -
 DR EMBL; M61100; AAA39310.1; -
 DR EMBL; S64082; AAA20265.1; -
 DR PIR; A44610; A44610.
 DR HSSP; P18510; IIR1.
 DR MGD; MGI:96547; IIR1.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 DR GlycoProtein; Signal; Alternative splicing.
 KW SIGNAL 1 26 BY SIMILARITY.
 FT CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST
 FT DISUFID 92 142 BY SIMILARITY.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC..) (POTENTIAL).
 FT VARSPIC 1 21 MEICWGPYSHLISLLILFPH -> MA (in isoform 2).
 FT FT /PRTid=VSP 002652.
 SQ SEQUENCE 178 AA; 20274 MW; 84AA002A3119C024 CRC64;
 Query Match 15.8%; Score 167; DB 1; Length 178;
 Best Local Similarity 31.1%; Pred. No. 1e-08;
 Matches 51; Conservative 26; Mismatches 75; Indels 12; Gaps 7;
 QY 28 NSALCGPKKKNLPPKFSHDDHKLVLVDSGNLIVAPDKYIR-PEIFPALLASSLSA 86
 DB 22 SEACRPSGKPKCKMQLFRMTDNTQKTFYRNQLA---GLQGNI--KLEEKIDMV 75
 QY 87 SAEKSPILLVKSGEFCYCDKQSHPSLQKKEKMLAKQESARPEIFYRAQV 146
 DB 76 PDLHS-VFGLHGKGLCLSCAKSGDI--KLQLEFVNITDLKNNEDGR-FTFIRSEK 131
 QY 147 GSMNMLESAHPGFWFICTSCNCPYGVTDKFNKRHI-EFSFQ 189
 DB 132 GPTTSFESAACPGWFLCTLEADRPVSLTNTPEEPILVTKFYFQ 175
 RESULT 10
 IL1A_MOUSE STANDARD; PRT; 152 AA.
 ID IL1A_MOUSE
 AC Q8R459;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin 1 family member 10 (IL-1F10).
 GN IL1F10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=1998051; PubMed=11991723;
 RA Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;
 RT "Genomic organization of the interleukin-1 locus.";
 RL Genome 79:726-733(2002).
 CC -1- FUNCTION: Binds soluble IL-1 receptor type 1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AY071844; AAL67155.1; -
 DR MGD; MGI:2652548; IL1F10.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
 DR Cytokine; MultiGene family.
 SQ SEQUENCE 152 AA; 17077 MW; 9AD03EB0C3C61D8A CRC64;
 Query Match 15.6%; Score 165.5; DB 1; Length 152;
 Best Local Similarity 33.6%; Pred. No. 1.2e-08;
 Matches 49; Conservative 18; Mismatches 72; Indels 7; Gaps 4;
 QY 45 FSIHDDHKLVLVDSGN-LIAPDKYIRPEIFPALLASSLSASAEKSPILLVSGE 103
 DB 10 YIIKDHAQALYTRNQLIGDDSDNYSPEKVCILPNGLDRSK---VPIFLMGSSGC 66
 QY 104 CYCDKDKQSHPSLQKKEKMLAKQESARPEIFYRAQVGSNMLESAHPGFWIC 163
 DB 67 CLACVATR--EGFLQLGEDVNIETDLKGEQGTTR-FTFORSIGSAFRLEAAACPGWFLC 123
 QY 164 TSCNCPYGVTDKFNKRHI-EFSFQ 189
 DB 124 GPAEPQAPQVLTKESEPSHTETFEYF 149
 RESULT 11
 IL1X_HUMAN STANDARD; PRT; 177 AA.
 ID IL1X_HUMAN
 AC P18510; Q14628; Q96GD6; Q9UPC0;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (ICIL-1RA) (IRAP) (IL-1RN).
 GN IL1RN OR IL1RA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=90220867; PubMed=2139180;
 RA Carter D.B., Deibel M.R., Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
 RA Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,
 RA Harris P.K.W., Yem A.W., Wazak G.A., Chosay J.G., Siew L.C.,
 RA Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinikson R.D.,
 RA Truesdell S.E., Shelly J.A., Bessalu T.E., Taylor B.M., Tracey D.E.;
 RT "Purification, cloning, expression and biological characterization of
 RT an interleukin-1 receptor antagonist protein.";
 RL Nature 344:633-638(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=90136921; PubMed=2137201;
 RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
 RA Hannum C.H., Thompson R.C.;
 RT "Primary structure and functional expression from complementary DNA
 RT of a human interleukin-1 receptor antagonist.";
 RL Nature 343:341-346(1990).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=91271363; PubMed=1828896;
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
 RA Brandhuber B.J., Thompson R.C.;
 RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
 RT gene family: evolution of a cytokine control mechanism.";

Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
 (4)
 RA SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=9233823; PubMed=1385987;
 RA Leonard A., Gorman P., Carrier M., Griffiths S., Scouney H.,
 RA Sheer D., Solari R.;
 RT "Cloning and chromosome mapping of the human interleukin-1 receptor
 RT antagonist gene.";
 RT Cytokine 4:83-89(1992).
 (5)
 RA SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 RX MEDLINE=9714604; PubMed=892991;
 RA Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
 RA Arend W.P., Smith M.F. Jr.;
 RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
 RT and inducible regulatory regions.";
 RT J. Immunol. 158:748-755(1997).
 (6)
 RA SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=91219436; PubMed=1827201;
 RA Haekill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
 RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.,
 RA "cDNA cloning of an intracellular form of the human interleukin 1
 RT receptor antagonist associated with epithelium.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
 (7)
 RA SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=95355865; PubMed=7829520;
 RA Muto M., Polentarutti N., Sironi M., Poli G., De Giola L.,
 RA Nicotra M., Mantovani A., Colotta F.;
 RT "Cloning and characterization of a new isoform of the interleukin 1
 RT receptor antagonist.";
 RT J. Exp. Med. 182:623-628(1995).
 (8)
 RA SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=95172072; PubMed=7867645;
 RA Kluemper R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshlyuk S., Carinci P., Prange C.,
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatirne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehly J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinaki M.I., Skalska U., Smalhus D.E.,
 RA Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 (10)
 RA SEQUENCE OF 26-45.
 RX MEDLINE=9035444; PubMed=2143761;
 RA Heindel P.L., Ames L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
 RT "Interleukin-1 receptor antagonist activity of a human interleukin-1
 RT inhibitor.";
 RT Nature 343:336-340(1990).
 (11)
 RA SEQUENCE OF 26-52.
 RX MEDLINE=9035444; PubMed=2143761;

Bienkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
 RA Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
 RA Heinkelson R.L., Chosay J.G., Tracey D.E.;
 RT "Purification and characterization of interleukin 1 receptor level
 RT antagonist proteins from THP-1 cells.";
 RT J. Biol. Chem. 265:14505-14511(1990).
 (12)
 RA SEQUENCE OF 35-177 FROM N.A. (ISOFORM 4).
 RX MEDLINE=98183404; PubMed=9514884;
 RA Weisbach L., Tran K., Colquhoun S.A., Champilaud M.F., Towle C.A.,
 RA "Detection of an interleukin-1 intracellular receptor antagonist mRNA
 RT variant.";
 RT Biochem. Biophys. Res. Commun. 244:91-95(1998).
 (13)
 RA STRUCTURE BY NMR.
 RX MEDLINE=92297633; PubMed=1534997;
 RA Stockman B.J., Scallil T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
 RA Brunner D.P., Yem A.W., Deibel M.R. Jr.;
 RT "Secondary structure and topology of interleukin-1 receptor
 RT antagonist protein determined by heteronuclear three-dimensional NMR
 RT spectroscopy.";
 RT Biochemistry 31:5237-5244(1992).
 (14)
 RA STRUCTURE BY NMR.
 RX MEDLINE=94320651; PubMed=8045306;
 RA Stockman B.J., Scallil T.A., Strakalaitis N.A., Brunner D.P.,
 RA Yem A.W., Deibel M.R. Jr.;
 RT "Solution structure of human interleukin-1 receptor antagonist
 RT protein.";
 RT FEBS Lett. 349:79-83(1994).
 (15)
 RA X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94230368; PubMed=8175703;
 RA Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
 RA Brandhuber B.J.;
 RT "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
 RT resolution.";
 RT J. Biol. Chem. 269:12874-12879(1994).
 (16)
 RA X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=95172072; PubMed=7867645;
 RA Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
 RA Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
 RT "Refined crystal structure of the interleukin-1 receptor antagonist.
 RT Presence of a disulfide link and a cis-proline.";
 RT Eur. J. Biochem. 227:838-847(1995).
 (17)
 RA X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
 RX MEDLINE=97215904; PubMed=9062194;
 RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
 RA Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;
 RT "A new cytokine-receptor binding mode revealed by the crystal
 RT structure of the IL-1 receptor with an antagonist.";
 RT Nature 386:194-200(1997).
 (18)
 RA FUNCTION: Inhibits the activity of IL-1 by binding to its
 RA receptor. Has no IL-1 like activity.
 (19)
 RA SUBCELLULAR LOCATION: Secreted (isoform 1). Cytoplasmic (isoforms
 RA 2, 3 and 4).
 (20)
 RA ALTERNATIVE PRODUCTS:
 RA Event=Alternative splicing; Named isoforms=4;
 RA Name=1;
 RA IsoId=P18510-1; Sequence=Displayed;
 RA Name=2; Synonyms=icIL-1ra; Sequence=VSP_002649;
 RA IsoId=P18510-2; Sequence=icIL-1ra type II;
 RA Name=3; Synonyms=icIL-1ra type II;
 RA IsoId=P18510-3; Sequence=VSP_002650;
 RA Name=4;
 RA IsoId=P18510-4; Sequence=VSP_002651;
 (21)
 RA TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
 RA PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
 (22)
 RA SIMILARITY: Belongs to the IL-1 family.
 (23)
 RA DATABASE: NMR=Red Systems' cytokine source book: IL1RN;
 RA WWW=http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=205".


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CC -----
DR EMBL; M56546; AAA59138.1; -
DR EMBL; M63099; AAB41943.1; -
DR EMBL; X52015; CA36262.1; -
DR EMBL; X53296; CAA37386.1; -
DR EMBL; X64532; CAA45832.1; -
DR U65590; AAB92268.1; -
DR EMBL; U65590; AAB92270.1; -
CC -----
Query Match 15.0%; Score 158.5; DB 1; Length 177;
Best Local Similarity 28.7%; Pred. No. 6.5e-08;
Matches 43; Conservative 30; Mismatches 66; Indels 11; Gaps 6;
QY 28 NSALCRGPKVKNLNPFKSIHDQHKVLVDGSLIAPVDKYYR-PEIFPALSSLSA 86
DB 21 SETICRPSGRKSSKKQAFRIWDVQKTFYLRNNQLVA----GYLGPNV--NLEBKIDVV 74
QY 87 SAEKGSPLILVSGKEPFLCYDCKKGGSHPSIOLKKEKMLTKLAQKESARRPTFYRAOV 146
DB 75 PIEPRA-FLGLHGKCKWLCLSCVKSDETR--LQLEAVNITLSENKQDKR-FAFIRSDS 130
QY 147 GSWNNLESAHPGWPFICTSCNCEPVGYT 176
DB 131 GPTTSFEBAACRGWFLCTAMEADQVSLTN 160
CC -----
RESULT 12
11FA_HUMAN STANDARD; PRT; 152 AA.
ID 11FA_HUMAN
AC 08RWZ1; Q969H5; Q9BYX1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-1 family member 10 (IL-1F10) (Interleukin-1 receptor
DE antagonist-like FcIL theta) (Interleukin-1 theta) (IL-1 theta) (FcIL
DE theta) (Interleukin-1 HY2) (IL-1HY2) (Interleukin-1 receptor
DE antagonist FKSG75).
GN IL1F10 OR FILIT OR IL1HY2 OR FKSG75.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thymus;
RX MEDLINE=21615180; PubMed=11747621;
RA Bensen J.T., Dawson P.A., Mychaleckyj J.C., Bowden D.W.;
RT "Identification of a novel human cytokine gene in the interleukin gene
RT cluster on chromosome 2q12-14."
RL J. Interferon Cytokine Res. 21:899-904(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fetal skin;
RX MEDLINE=21282953; PubMed=11278614;
RA Lin H., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussell J.,
RA Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
RT "Cloning and characterization of IL1HY2, a novel interleukin-1 family
RT member."
RL J. Biol. Chem. 276:20597-20602(2001).

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RN  VARIANTS THR-44 AND ASP-51.
RP
RX  MEDLINE=21986051; PubMed=11991723;
RA  Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
RT  "Genomic Organization of the Interleukin-1 locus."
RL  Genomics 79:726-733 (2002).
CC  -1- FUNCTION: Binds soluble IL-1 receptor type 1.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=Q8MWZ1-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q8MWZ1-2; Sequence=VSP_002658;
CC      Note=No experimental confirmation available;
CC      -1- TISSUE SPECIFICITY: Expressed in fetal skin, spleen and tonsil.
CC      Expressed mostly in the basal epithelia of skin and in
CC      proliferating B cells of the tonsil.
CC      -1- SIMILARITY: Belongs to the IL-1 family.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AY029413; AAK33010.1; -
DR  EMBL; AY026753; AAK01948.1; -
DR  EMBL; AF344755; AAK01948.1; -
DR  EMBL; AF344756; AAK68049.1; -
DR  Genew; HGNC:15552; IL1P10.
DR  InterPro; IPR008966; CytoK_IL1_like.
DR  InterPro; IPR000975; Interleukin_1.
DR  Pfam; PF00340; IL1; 1.
DR  ProDom; PD002536; Interleukin_1; 1.
DR  SMART; SMO0125; IL1; 1.
DR  PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
DR  CytoKine; MultiGene Family; Alternative splicing, Polymorphism.
FT  FT  9
FT  VARSPLIC
FT  VARIANT 44 44
FT  VARIANT 51 51
FT  SEQUENCE 152 AA; 16943 MW; E0ABD2496551B34F CRC64;
SQ
Query Match 14.8%; Score 156.5; DB 1; Length 152;
Best Local Similarity 28.3%; Pred. No. 8.4e-08;
Matches 43; Conservative 30; Mismatches 50; Indels 29; Gaps 5;
QY 46 SIHQDQKRVLTLD-----SGNLIAVPDDKVIIRPEIFALASSLSASAEKGSPIILGV 98
DB 19 ALYTRDQGLVGDVDVANCCEAKKCIIPNGRLATKY-----PIFLGI 61
QY 99 SKGEFCIYC-DKDKGQSHPSIQLKKEKIMKILAAQKESARPRFTYYRAOVSGMNLESA 157
DB 62 QGGSGRCIACVETTEGG--PSIQLDVANIIEELYKGGEEATR-FTFPGSSGSAFRLAAAW 117
QY 158 PGWFICTSCNENVEVGTDKRENKRIIEFSQ 189
DB 118 PGWFLCGPAEPQDPVQLTKESEPSARTKTFYE 149

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DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL1RA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=94165101; PubMed=7509813;
RA Cominelli F., Borcolami M., Pizarro T.T., Monsacchi L., Ferretti M.,
RA Brewer M.T., Eisenberg S.P., Ng R.K.;
RT "Rabbit interleukin-1 receptor antagonist. Cloning, expression,
RT functional characterization, and regulation during intestinal
RT inflammation.";
RL J. Biol. Chem. 269:6962-6971(1994).
RN (2)
RP SEQUENCE FROM N.A.
RA Hamada H., Mulligan R.C.;
RL Submitted (XXX-1992) to the EMBL/Genbank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RA MEDLINE=93052512; PubMed=1427977;
RA Goto F., Goto K., Miyata T., Ohkawara S., Takao T., Mori S.,
RA Furukawa S., Maeda T., Iwanaga S., Shimonishi Y., Yoshinaga M.;
RT "Interleukin-1 receptor antagonist in inflammatory exudate cells of
RT rabbits. Production, purification and determination of primary
RT structure.";
RL Immunology 77:235-244(1992).
CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
CC receptor. Has no IL-1 like activity.
CC -1- SUBCELLULAR LOCATION: Secreted (by similarity).
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC -----
DR EMBL; S68977; AAB30093.1; -;
DR EMBL; M57526; AAB31374.1; -;
DR EMBL; D21832; BAA04860.1; -;
DR PIR; A54377; A54377.
DR HSSP; P18510; IL1R.
DR InterPro; IPR008996; CytoK IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KM Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 177 BY SIMILARITY.
FT INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 177 AA; 20214 MM; F5BC087F097FEFAF CRC64;
Query Match 14.6%; Score 154.5; DB 1; Length 177;
Best Local Similarity 27.0%; Pred. No. 1.6e-07;
Matches 44; Conservative 23; Mismatches 51; Indels 45; Gaps 6;
QY 32 CRGPKVKNLPKRSIHQDHKVLVDSGNLIA-----VDDKNYIRPEI 75
DB 25 CRPGKRCPCRMQARINDVQNKTFYLRNNQVAGYLGCPNKLKEERIDVP---IEPOL 80
QY 76 PFALASSLSASAEKSPILIGVSKGEFCYCDK--DKGSHPSLQKKEKMLAAQKE 133
DB 81 LF-----LGIGRKLCLSCVSGDKMKLH---LEAVNITDLGNKE 118

QY 134 SARPPFIYRAQVGSMMLESAPHGWFICTSCNCEPVGVD 176
DB 119 QDKR-FTFIRNSGPTTFESASCPCWFLCTALADQPVSLTN 160
RESULT 14.
ID IL1X BOVIN STANDARD; PRT; 174 AA.
AC 077482.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IL-1RN)
DE (IRAP).
GN IL1RN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=98305607; PubMed=9643454;
RA Kirisawa R., Fukuda T., Yamana H., Hagiwara K., Goto M., Obata Y.,
RA Yoshino T., Iwai H.;
RT "Enzymatic amplification and expression of bovine interleukin-1
RT receptor antagonist cDNA.";
RL Vet. Immunol. Immunopathol. 62:197-208(1998).
CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
CC receptor. Has no IL-1 like activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; AB005148; BAA31854.1; -;
DR HSSP; P18510; IL1R.
DR InterPro; IPR008996; CytoK IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KM Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 174 BY SIMILARITY.
FT INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 89 139 BY SIMILARITY.
FT CARBOHYD 107 107 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 174 AA; 19926 MM; 1B56E7F224FF851F CRC64;
Query Match 14.4%; Score 152; DB 1; Length 174;
Best Local Similarity 29.6%; Pred. No. 2.6e-07;
Matches 48; Conservative 18; Mismatches 54; Indels 42; Gaps 6;
QY 45 PSIHDDHKVLVDSGNLIA-----VDDKNYIRPEIFPALASSLSASA 88
DB 36 FRIMDVQKIFRYLRNNQVAGYLGCPNKLKEERIDVP---IEPHTMF----- 80
QY 89 EKSPILIGVSKGEFCYCDKDGSHPSLQKKEKMLAAQESARPPFIYRAQVGS 148
DB 81 -----LGIHGKLCIACVKSDEI--KLTAVNITDLNQNREDDKR--FAFIRFNGP 130
QY 149 MNMLESAAPHGWFICTSCNCEPVGVD--KFNKRKHIEFSQ 189
DB 131 TTSFESAACPGWFLCTSLADQPVGLTNMPTALVKTKFFQ 172

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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:20:54 ; Search time 40 Seconds
(without alignments)
488.172 Million cell updates/sec

Title: US-09-869-566-5
Perfect score: 1059
Sequence: 1 MSALLILALYGAAYADYKD.....IEFSFQPVCKAEMSPSEVSD 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174.5	16.5	155	2 JC7104	interleukin-1 rece
2	167	15.2	178	2 A44610	interleukin-1 rece
3	161	15.0	180	2 A39386	interleukin-1 rece
4	158.5	14.6	177	2 A30368	interleukin-1 rece
5	154.5	14.6	177	2 A54377	interleukin-1 rece
6	146.5	13.8	178	2 C40956	interleukin-1 rece
7	131.5	12.4	266	1 S23010	interleukin-1 beta
8	128	12.1	267	2 S38373	interleukin-1 beta
9	121.5	11.5	267	1 JN0724	interleukin-1 beta
10	120.5	11.4	269	1 I55969	interleukin-1 beta
11	118	11.1	266	1 ICBO1B	interleukin-1 beta
12	98	9.3	269	1 ICHUB1	interleukin-1 beta
13	95.5	9.0	246	2 B25528	trypsin (EC 3.4.21
14	92.5	8.7	268	1 A30584	interleukin-1 beta
15	91	8.6	404	2 S34031	KRX3 protein - yea
16	89.5	8.5	214	2 JC5646	interleukin-1 beta
17	84	7.9	270	1 ICMS1	interleukin-1 aliph
18	83.5	7.9	776	2 S67053	probable membrane
19	82.5	7.8	246	1 TPRRT1	trypsin (EC 3.4.21
20	82	7.7	513	2 T17806	probable flavoprot
21	81	7.6	320	2 A81434	molybdenum cofacto
22	81	7.6	914	2 B96592	hypothetical prote
23	80.5	7.6	246	1 TRRT2	trypsin (EC 3.4.21
24	80.5	7.6	845	2 T17291	hypothetical prote
25	78.5	7.4	244	2 E70224	hypothetical prote
26	78	7.4	1277	2 E70224	hypothetical prote
27	77	7.3	859	2 C87358	hypothetical prote
28	76.5	7.2	231	2 S59589	histone H1 - Chlam
29	76.5	7.2	375	2 F70151	protein-glutamate

30	76.5	7.2	571	2 D86164	hypothetical prote
31	76.5	7.2	627	2 T02846	dynein light chain
32	76	7.2	425	2 T24522	hypothetical prote
33	76	7.2	448	2 JN0118	glucan 1,3-beta-gl
34	75.5	7.1	436	2 AH1387	cell wall binding
35	75.5	7.1	247	1 TRDG	trypsin (EC 3.4.21
36	75	7.1	247	2 S13813	trypsin (EC 3.4.21
37	75	7.1	247	2 S12764	trypsin (EC 3.4.21
38	75	7.1	314	2 T44311	ADPglyceromanno-he
39	75	7.1	334	2 T34326	homeobox and LIM d
40	74.5	7.0	221	2 F84148	hypothetical prote
41	74.5	7.0	270	1 S10532	interleukin-1 aliph
42	74.5	7.0	504	1 VCPV3A	coat protein - ade
43	74.5	7.0	1116	2 T31432	K-C1 cotransport p
44	74.5	7.0	1199	2 T15826	hypothetical prote
45	74	7.0	728	2 B81370	phosphoribosylform

ALIGNMENTS

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RESULT 1
JC7104
Interleukin-1 receptor antagonist - human
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: JC7104
R:Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford, J
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A:Title: IL1H1: A novel interleukin-1 receptor antagonist gene.
A:Reference number: JC7104; MUID:99443727; PMID:10512743
A:Accession: JC7104
A:Molecule type: mRNA
A:Residues: 1-155 <MULT>
A:Cross-references: GB:A186094; NID:G6049804; PID:AAF02757.1; PID:G6049805
C:Genetics:
A:Gene: il1h1
A:Map position: 2q14
A:Keywords: macrophage

Query Match      16.5%  Score 174.5; DB 2; Length 155;
Best Local Similarity 32.0%; Pred. No. 4,7e-09;
Matches 54; Conservative 18; Mismatches 48; Indels 49; Gaps 7;

Oy 28 NSALCRGPKVKNLNPKEFISHDQKTVLVDSGLVAVPDKNYRPRIFPALASISAS 87
Db 4 SGALC-----FRMKDSALKVLYLHNNQL-----LAGLHAGK 35

Oy 88 AEKG-----SPILLGVSGEFCLYCDKDGQSHPSLOLKEKLMKL-AAQ 131
Db 36 VIKKEEISVVPNRMLDASLSPVILGVGGSGCLSC--GVGQ-EPTLYLEPYNIMELYIGA 92

Oy 132 KESARPFPIFYRAQVGSMMMLESAHPGWFTICSCNCPYGVTDKREN 180
Db 93 KES--KSFTEFYRDMGLTSSFESAAYPGWFLCTVPEADQPRYLQLPEN 139

RESULT 2
A44610
Interleukin-1 receptor antagonist precursor - mouse
N:Alternate names: IL-1Ra
C:Species: Mus musculus (house mouse)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C:Accession: A44610; B40956; A49031; I56106; I52970
R:Matsushime, H.; Rousset, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 79, 616-623, 1991
A:Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrophage
A:Reference number: A44610; MUID:91316273; PMID:1830498
A:Accession: A44610
A:Molecule type: mRNA
A:Residues: 1-178 <MAT>
A:Cross-references: GB:M64404; NID:G198296; PIDN:AAA39277.1; PID:G198297
R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
```

Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
 A/Title: Interleukin-1 receptor antagonist is a member of the interleukin-1 gene family:
 A/Reference number: A40956; MUID:91271363; PMID:1828896
 A/Accession: B40956
 A/Molecule type: DNA
 A/Residues: 7-178 <RES>
 A/Cross-references: GB:M63100; NID:g198389; PIDN:AAA9310.1; PID:g198390
 R/Shukla, M.E.; Essalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
 Eur. J. Immunol. 21, 2775-2780, 1991
 A/Title: Cloning, heterologous expression and characterization of murine interleukin-1
 A/Reference number: A49031; MUID:92037824; PMID:1834470
 A/Accession: A49031
 A/Molecule type: mRNA
 A/Residues: 23-178 <SHU>
 A/Cross-references: GB:M74294; NID:g198387; PIDN:AAA9309.1; PID:g198385
 A/Experimental source: peritoneal macrophages, ICR strain
 A/Note: Sequence extracted from NCBI Backbone (NCBI:4082, NCBI:64085)
 R/Zahedi, K.; Seidlin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
 J. Immunol. 146, 4228-4233, 1991
 A/Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map
 A/Reference number: I56106; MUID:91250712; PMID:1828262
 A/Accession: I56106
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Residues: 1-178 <RES>
 A/Cross-references: GB:M74294; NID:g198387; PIDN:AAA9309.1; PID:g198388
 R/Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
 Cytokine 6, 1-9, 1994
 A/Title: The mouse interleukin-1 receptor antagonist protein: gene structure and regulat
 A/Reference number: I52970; MUID:94271931; PMID:8003626
 A/Accession: I52970
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-178 <RES>
 A/Cross-references: GB:U32838; NID:g487864; PIDN:AAA20576.1; PID:g528978
 C/Genetics:
 A/Gene: IL-1rn
 A/Introns: 40/2; 70/1; 107/3
 C/Superfamily: interleukin-1
 C/Keywords: cytokine receptor
 F/1-26/Domain: signal sequence #status predicted <SIG>
 F/1-26/Product: interleukin-1 receptor antagonist #status predicted <MA>
 F/2-178/Product: interleukin-1 receptor antagonist #status predicted <MA>
 Query Match 15.8%; Score 167; DB 2; Length 178;
 Best Local Similarity 31.1%; Pred. No. 2.8e-08;
 Matches 51; Conservative 26; Mismatches 75; Indels 12; Gaps 7;
 QY 28 NSALCRGPVKYNLPKFFSIHDDHKLVLDSGNLIVDPKNYIR-DEIFPALASSLSA 86
 Db 22 SEAACRPSGRKPCMQAFRIWDTNQTFYLRNQLIA---GYLQGPNI--KLEEKIDMV 75
 QY 87 SAEKGSPIILGVSGEFCVCDKDKGSHPSLQKKRKLAAQKSARRPFIFYAQV 146
 Db 76 PIDLHS-VFPIGHGKCLCLCAKSGDDI--KLQLEEVNITDLSKNEKEDR-FTFIRSEK 131
 QY 147 GSNMLESAAHPGFICTSCNCPVGVTDKFEKRIH-EESFO 189
 Db 132 GPITTSFSAACPGMFLCTTLEADRFVSLINPEPPLIVTYFYFO 175
 RESULT 3
 A39386
 Interleukin-1 receptor antagonist, long intracellular splice form - human
 N/Contains: Interleukin-1 receptor antagonist, short intracellular splice form
 C/Species: Homo sapiens (man)
 C/Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
 C/Accession: I37893; A39386
 R/Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovani
 J. Exp. Med. 182, 623-628, 1995
 A/Title: Cloning and characterization of a new isoform of the interleukin-1 receptor and
 A/Reference number: I37893; MUID:95355865; PMID:7629520
 A/Accession: I37893
 A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA
 A/Residues: 1-180 <RES>
 A/Cross-references: EMBL:X84348; NID:g1008970; PIDN:CAA59087.1; PID:g1008971
 R/Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.D.;
 Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
 A/Title: cDNA cloning of an intracellular form of the human interleukin-1 receptor antagc
 A/Reference number: A39386; MUID:91219436; PMID:1827201
 A/Accession: A39386
 A/Molecule type: mRNA
 A/Residues: 1-3, 25-180 <HAS>
 A/Cross-references: GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:g186292
 C/Comment: for an alternative splice form, see PIR:A30368
 C/Genetics:
 A/Gene: GDB:IL1RN
 A/Cross-references: GDB:125897; OMIM:147679
 A/Map position: 2q14.2-2q14.2
 C/Superfamily: interleukin-1
 C/Keywords: alternative splicing; cytokine receptor
 F/1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form
 F/1-3, 25-180/Product: interleukin-1 receptor antagonist, short intracellular splice form
 Query Match 15.2%; Score 161; DB 2; Length 180;
 Best Local Similarity 27.9%; Pred. No. 1e-07;
 Matches 48; Conservative 35; Mismatches 71; Indels 18; Gaps 8;
 QY 13 AVAD-YKD-----DDKTLAANSALCRGPVKYNLPKFFSIHDDHKLVLDSGNLIV 65
 Db 2 ALADLYEBEGGGGGBEDNADSKETICRPSGRSSKQAFRIWDTNQTFYLRNQLVA- 60
 QY 66 PDKNYIR-DEIFPALASSLSASAEKSPILLGVSGEFCVCDKDKGSHPSLQKKR 124
 Db 61 ---GYLQGPNI--NLEEKIDVPIEIPA-LFLGIGHGKXCLSCVKSQDETR--LQLEAVN 112
 QY 125 LMKLAQKSARRPFIFYAQVGSNMLESAAHPGFICTSCNCPVGVTD 176
 Db 113 ITDLSNRKQDKR-FAPIRSDSGPTTSFSAACPGMFLCTTLEADQPVSLIN 163
 RESULT 4
 A30368
 Interleukin-1 receptor antagonist secreted form precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000
 C/Accession: A40956; I37894; A30368; S08160; S08159; A37822
 R/Bisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
 Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
 A/Title: Interleukin-1 receptor antagonist is a member of the interleukin-1 gene family:
 A/Reference number: A40956; MUID:91271363; PMID:1828896
 A/Accession: A40956
 A/Molecule type: DNA
 A/Residues: 1-177 <RES>
 A/Cross-references: GB:M63109; NID:g186385; PIDN:AAA1943.1; PID:g186386
 R/Lennard, A.; Gorman, P.; Carriere, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari, R.
 Cytokine 4, 83-89, 1992
 A/Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist ge
 A/Reference number: I37894; MUID:92338323; PMID:1385887
 A/Accession: I37894
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-177 <LEN>
 A/Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799
 J. Carter, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, J.
 R.G.; Siew, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; Tr
 Nature 344, 633-638, 1990
 A/Title: Purification, cloning, expression and biological characterization of an interlev
 A/Reference number: A30368; MUID:9020867; PMID:2139180
 A/Accession: A30368
 A/Molecule type: mRNA
 A/Residues: 1-177 <CAR>
 A/Cross-references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579
 A/Note: parts of this sequence, including the amino end of the mature protein, were confi
 R/Bisenberg, S.P.; Evans, R.U.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.; J
 Nature 343, 341-346, 1990

A/Title: Primary structure and functional expression from complementary DNA of a human
A/Reference number: S08160; MUID:90136921; PMID:2137201
A/Accession: S08160
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-177 <E12>
A/Cross-references: GB:X52015; NID:G32576; PIDN:CA56262.1; PID:G32577
R:Hannun, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Driggs, D.J.; Heimdal, P.L.; At
Nature 343, 336-340, 1990
A/Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.
A/Reference number: S08159; MUID:90136920; PMID:2137200
A/Accession: S08159
A/Molecule type: protein
A/Residues: 26-75; 97-108; 110-116; 120-131; 163-176 <HAN>
R:Blenkowiak, M.J.; Bessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde,
J. Biol. Chem. 265, 14505-14511, 1990
A/Title: Purification and characterization of interleukin 1 receptor level antagonist pr
A/Reference number: A37822; MUID:90354444; PMID:2143761
A/Accession: A37822
A/Molecule type: protein
A/Residues: 26-52; 70-77; 122-127; 170-175 <BIE>
A/Experimental source: culture medium, PMA-stimulated THP-1 cells
C/Comment: For an alternative splice form, see PIR:A39386
C/Genetics:
A/Gene: GDB:IL1RN
A/Cross-references: GDB:125897; OMIM:147679
A/Map position: 2q14.2-q14.2
A/Intons: 39/2; 69/1; 106/3
C/Superfamily: interleukin-1
C/Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:129/Protein: interleukin-1 receptor antagonist #status experimental <MAT>
F:109/Binding site: carbohydrate (Asn) (covalent) #status experimental

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Best Local Similarity 28.7%; Pred. No. 1.8e-07;
Matches 43; Conservative 30; Mismatches 66; Indels 11; Gaps 6;

Qy 28 NSALCRGPKVKNLPPKFSIHDOHKVLVLDGSLIAVPDKNYR-PIFFALASSLSA 86
Db 21 SETICRPSGRKSSKQAFRIWDVQKTFYLRNNQLVA---GYLQGPVNV--NLEEKIDIV 74

Qy 87 SAEKSPILIGVSGEPLCYCDKXGSHPSLOLKKKMLKLAQKESARPPFIYRAQV 146
Db 75 PIEPHA-LFGLIHGKCKLCSVKSQDEIR--LQLEAVNITDLSNRKQDKR-FAFIRSDS 130

Qy 147 GSMNMLSAHPGWFICTSCNCPNPGVTD 176
Db 131 GPTTFESAACPGWFLCTAMADQPVSLTN 160

RESULT 5
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interleukin-1 receptor antagonist secreted form precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
A/Accession: A54377; 146729
R:Cominelli, F.; Borcolami, M.; Piarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.T.
J. Biol. Chem. 269, 6962-6971, 1994
A/Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional chara
A/Reference number: A54377; MUID:94165101; PMID:7509813
A/Accession: A54377
A/Molecule type: mRNA
A/Residues: 1-177 <COM>
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A/Experimental source: colon tissue
A/Note: sequence extracted from NCI backbone (NCBI:144168, NCBI:P.144169)
R:Goto, F.; Goto, K.; Miyata, T.; Okawara, S.; Takeo, T.; Mori, S.; Furukawa, S.; Maeda
Immunology 77, 235-244, 1992
A/Title: Interleukin-1 receptor antagonist in inflammatory exudate cells of rabbits. Proc
A/Reference number: 146729; MUID:93052512; PMID:1427977
A/Accession: 146729
A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-177 <GOT>
A/Cross-references: GB:D21832; NID:G425787; PIDN:BA04860.1; PID:G452205
C/Superfamily: interleukin-1
C/Keywords: cytokine receptor; extracellular protein; glycoprotein
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F:109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.6%; Score 154.5; DB 2; Length 177;
Best Local Similarity 27.0%; Pred. No. 4.2e-07;
Matches 44; Conservative 23; Mismatches 51; Indels 45; Gaps 6;

Qy 32 CRGPKVKNLPPKFSIHDOHKVLVLDGSLIA-----VDPKNYIRPEI 75
Db 25 CRGPKVKNLPPKFSIHDOHKVLVLDGSLIA-----VDPKNYIRPEI 75

Qy 76 FFALASSLSASAEKSPILIGVSGEPLCYCDKXGSHPSLOLKKKMLKLAQKE 133
Db 81 LF-----LGIRGKLCISCVSGDKMLH-----LEAVNITDLGNKE 118

Qy 134 SARPPFIYRAQVGSMMNMLSAHPGWFICTSCNCPNPGVTD 176
Db 119 QDKR-FTFIRNSGPTTFESASCPGWFLCTALADQPVSLTN 160

RESULT 6
A40956
interleukin-1 receptor antagonist precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
A/Accession: A40956
R:Eisenberg, S.P.; Brewer, M.T.; Verdier, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A/Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A/Reference number: A40956; MUID:91271363; PMID:1828896
A/Accession: A40956
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-178 <E15>
A/Cross-references: GB:M63101; NID:G204928; PIDN:AAA41434.1; PID:G204929
C/Superfamily: interleukin-1
C/Keywords: cytokine receptor

Query Match 13.8%; Score 146.5; DB 2; Length 178;
Best Local Similarity 26.6%; Pred. No. 2.4e-06;
Matches 47; Conservative 23; Mismatches 58; Indels 49; Gaps 6;

Qy 31 LCRGPKVKNL-----PKK---FSIHDOHKVLVLDGSLIA----- 64
Db 3 ICRGPKVSHLISLILILFRBSAGHPGKRPCKMQAFRIWDVQKTFYLRNNQLAGYLQ 62

Qy 65 ----VDPKNYIRPEIFALASSLSASAEKSPILIGVSGEPLCYCDKXGSHPSLO 119
Db 63 GPNKLEKIDWVIDP-----RNVPFGIHGKCLCSVSGDDT--KLQ 105

Qy 120 LKKEKMLKLAQKESARPPFIYRAQVGSMMNMLSAHPGWFICTSCNCPNPGVTD 176
Db 106 LEEVNTDLNKKKEDEKR-FTFIRSETGPTTFESASCPGWFLCTTLEADHPVSLTN 161

RESULT 7
S23010
interleukin-1 beta precursor - sheep
N/Alternate names: hematopoietin-1; IL-1 beta
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
A/Accession: S23010; S43047; S133092; B61246
R:Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A/Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A/Reference number: S23010; MUID:92119335; PMID:1840515
A/Accession: S23010
A/Molecule type: mRNA

A/Residues: 1-266 <SEO>

A/Cross-references: EMBL:X56972; NID:G1808; PIDN:CAA0293.1; PID:G1809

A/Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an additional R;Sargan, D.R. The EMBL Data Library, May 1992

A/Reference number: S43047

A/Accession: S43047

A/Molecule type: mRNA

A/Residues: 1-113, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'L', 146-266 <SAR>

A/Cross-references: EMBL:X54796; NID:G1273; PIDN:CAA38566.1; PID:G1274

R;Fiskersstrand, C.; Sargan, D.

Nucleic Acids Res. 18, 7165, 1990

A/Title: Nucleotide sequence of ovine interleukin-1 beta.

A/Reference number: S13092; MUID:91088326; PMID:2263490

A/Accession: S13092

A/Molecule type: mRNA

A/Residues: 1-113, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'L', 146-266 <FTS>

A/Cross-references: EMBL:X54796

A/Note: the authors translated the codon AGT for residue 62 as Arg

R;Andrews, A.E.; Barham, G.J.; Brandon, M.R.; Nash, A.D.

Immunology 74, 453-460, 1991

A/Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.

A/Reference number: A61246; MUID:92120716; PMID:1769692

A/Accession: B61246

A/Molecule type: mRNA

C/Comment: This protein lacks a conventional signal sequence for protein export. Cleaved form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.

C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a

C/Genetic:

A/Gene: IL-1-beta

C/Superfamily: Interleukin-1

C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen

F;114-266/Product: interleukin-1 beta #status predicted <MAT>

Query Match 12.4%; Score 131.5; DB 1; Length 266;

Best Local Similarity 27.2%; Pred. No. 9,7e-05;

Matches 44; Conservative 30; Mismatches 63; Indels 25; Gaps 8;

QY 17 YKDDDKL---AAANSALCGPKVKNLPPKFSIHODHVLVLDG---NLAVDPKXY 70

Db 103 FETSSBELLDAAVQVSKK-----LDDEQKSLVLDSPCVKALHLPSQEM 149

QY 71 IREIFPALASSLSAESAEGSPILLGVSKGEFLCYDKQGSHPISLQKKEKMLGLAA 130

Db 150 SR-EVVFPCW-SFVQGEKDKKIFVALGIRDKNLYLSGVK-KGDT-PTLQ--EVDPKXY 203

QY 131 QKESARRPFIYRAOVGSNNMLESAAHPGFICTSCNCEPV 172

Db 204 PKENMEKRFVFKTEIKNTVEFESVLYPNWYISTQAEKPV 245

RESULT 8

S38373

Interleukin-1 beta precursor - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999

R;Vandenbrouck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Opde

Eur. J. Biochem. 217, 45-52, 1993

A/Title: Gene sequence, cDNA construction, expression in *Escherichia coli* and geneticall

A/Reference number: S38373; MUID:94039070; PMID:8223564

A/Accession: S38373

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-267 <VAN>

A/Cross-references: EMBL:X74568; NID:9407899; PIDN:CAA52660.1; PID:9407900

C/Genetic:

A/Insertions: 16/2; 33/3; 99/1; 154/1; 197/3

C/Superfamily: Interleukin-1

Query Match 12.1%; Score 128; DB 2; Length 267;

Best Local Similarity 28.9%; Pred. No. 0.00021;

Matches 43; Conservative 28; Mismatches 66; Indels 12; Gaps 6;

QY 27 ANSALGRGKVKNNLPPKFSIHODHVLVLDGNTLAVPD--KNYIRPEIFALASSLS 84

Db 107 ANGFLDAPVQSVQDK---LQDKDEKALVGLPHEKRLHLKGLKREVFQMSFVQ 163

QY 85 SASAERKSPILLGVSKGEFLCYC-DKDKQGSHPISLQKKEKMLAAQESARRPFIYR 143

Db 164 DSDGDK-IVTLGIGKKNLYLSGVKMD---DPTLQL--EVDPKSYPRDKMEKRFVFK 217

QY 144 AOVGSNNMLESAAHPGFICTSCNCEPV 172

Db 218 TEIKNVEFESVLYPNWYISTQAEKPV 246

RESULT 9

JN0724

Interleukin-1 beta precursor - pig

N/Alternate names: hematopoietin-1; IL-1 beta

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999

C/Accession: JN0724

R;Hether, M.J.; Lin, G.; Smith, D.M.; Murrugh, M.P.; Mollitor, T.W.

Gene 129, 285-289, 1993

A/Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 bet

A/Reference number: JN0724; MUID:93314975; PMID:8325511

A/Accession: JN0724

A/Molecule type: mRNA

A/Residues: 1-267 <HUB>

A/Cross-references: GB:M86725; NID:G164607; PIDN:AAA02584.1; PID:G164608

A/Experimental source: alveolar macrophage

C/Comment: This protein is a pleiotropic cytokine that mediates a variety of processes in

C/Comment: This protein lacks a conventional signal sequence for protein export. Cleavage

ved form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.

C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a

C/Superfamily: Interleukin-1

C/Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage

F;115-267/Product: interleukin-1 beta #status predicted <ILI>

F;77/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 11.5%; Score 121.5; DB 1; Length 267;

Best Local Similarity 25.9%; Pred. No. 0.00084;

Matches 44; Conservative 28; Mismatches 73; Indels 25; Gaps 7;

QY 19 DDDDK-----LAANSALCGPKVKNLPPKFSIHODHVLVLDGNTLAV 65

Db 86 DDDQKSIFFSFIIEEPIILETCNDPVCANVQSWCK---LQDKHKSILVAGPMGLA 142

QY 66 PD--KNYIRPEIFALASSLSAESAEGSPILLGVSKGEFLCYC-DKDKQGSHPISLQK 122

Db 143 LHLTGDLKREVFQW-SFVQGDSDSNKIPVTLGIGKKNLYLSGVKMD---NPTLQL-- 196

QY 123 EKIMKLAQESARRPFIYRAOVGSNNMLESAAHPGFICTSCNCEPV 172

Db 197 EDIDPKRYPKRDMEKRFVFKTEIKNVEFESVLYPNWYISTQAEKPV 246

RESULT 10

I55969

Interleukin-1 beta precursor - mouse

N/Alternate names: hematopoietin-1; IL-1 beta

C/Species: Mus musculus (house mouse)

C/Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999

C/Accession: I55969; A24719; S13029

R;Gray, P.W.; Glaister, D.; Chen, E.; Goeddel, D.V.; Pennica, D.

J. Immunol. 137, 3644-3648, 1986

A/Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for mu

A/Reference number: I55969; MUID:87058957; PMID:3491144

A/Accession: I55969

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-269 <RES>

A/Cross-references: GB:M15131; NID:G198293; PIDN:AAA9276.1; PID:G309398

	Query Match	11.4%	Score 120.5	DB 1	Length 269
	Best Local Similarity	27.8%	Pred. No. 0.0011		
	Matches	50	Conservative	34	Mismatches 79
					Indels 17
					Gaps 9
Qy	14	VADYKDDDDKLAANASALCRGPKVKNLPPKPSIHDQHKVLVL-DSGNLAIAP-DKNYI	71		
Db	103	LCDSWDSDDD-----NLIVCDVP-IRQLH---YRLDEQKSLVSDPYELKALHNGONI	153		
Qy	72	RPEIFPALASSLSASAEKGSPIILGVSKGFCLYCDQKQSHPSIQLKXKMLKLAQ	131		
		::: :: ::	::: :: ::	::: :: ::	
Db	154	NQGYIFSKSPVQGEPSNDK-IPVALGLKGNLYLSCVWKDGT--PTQL--ESVDPKQY	208		
		::: :: ::	::: :: ::	::: :: ::	
Qy	132	KESARPRPIIFRAQVGSNNMLSEAAHPQWIFCTSGNCNEPVGVDKPNRKHIEFSFPV	191		
		::: :: ::	::: :: ::	::: :: ::	
Db	209	KKKWEKRFVFNKIEVKSIVEFESAEPFPMVYISTSAEKKPVFLGN--SGQDIIIDFTWESV	267		
		::: :: ::	::: :: ::	::: :: ::	

RESULT 12
 ICHUIB
 interleukin-1 beta precursor [validated] - human
 N/Alternate names: hematopoietin-1; IL-1 beta
 C/Species: Homo sapiens (man)
 C/Date: 28-Feb-1996 #sequence revision 15-May-1998 #text change 15-Sep-2000
 A/Accession: A25542 #28019; A94023; A93361; I51852; I65500; I38132; B27616; A01848; S19
 R/Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Aaron, P.E.
 Nucleic Acids Res. 14, 7897-7914, 1986
 A/Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev
 A/Reference number: A25542; MUID:87040762; PMID:3490654
 A/Accession: A25542
 A/Molecule type: DNA; mRNA
 A/Residues: 1-5,'K','7-269 <C1A>
 A/Cross-references: GB:X04500; NID:G33788
 A/Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu
 A/Bernst, G.; Raugel, G.; Palla, E.; Carinici, V.; Buonamassa, D.T.; Meili, M.
 Gene 52, 95-101, 1987
 A/Title: Human interleukin-1 beta gene.
 A/Reference number: A29019; MUID:87248099; PMID:2254882
 A/Accession: A29019

A:Cross-references: GB:M54333; NID:G186287; PIDN:AAA59136.1; PID:G186288
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A:Reference number: A94023; PMID:85088517; PMID:6083565
A:Accession: A94023
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-269 <AUR>
A:Cross-references: GB:K02370; NID:G186268; PIDN:AAA6106.1; PID:G307043
R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gallie, S.
Nature 315, 641-647, 1995
A:Title: Cloning, sequence and expression of two distinct human interleukin-1 complement
A:Reference number: A93361; PMID:85240547; PMID:2389698
A:Accession: A93361
A:Molecule type: mRNA
A:Residues: 1-269 <MAR>
A:Cross-references: GB:K02532; NID:G33789; PIDN:CAA26372.1; PID:G33790
A:Note: parts of this sequence, including the amino end of the mature form, were confirmed
R:Webb, A.C.; DiPaello, C.A.; Rosenmasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au
Adv. Gene Technol. 22, 339-340, 1985
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A:Reference number: I51852
A:Accession: I51852
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Cross-references: GB:M54333; NID:G186287; PIDN:AAA59136.1; PID:G186288
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A:Reference number: A94023; PMID:85088517; PMID:6083565
A:Accession: A94023
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-269 <AUR>
A:Cross-references: GB:K02370; NID:G186268; PIDN:AAA6106.1; PID:G307043
R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gallie, S.
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A:Reference number: A93361; PMID:85240547; PMID:2389698
A:Accession: A93361
A:Molecule type: mRNA
A:Residues: 1-269 <MAR>
A:Cross-references: GB:K02532; NID:G33789; PIDN:CAA26372.1; PID:G33790
A:Note: parts of this sequence, including the amino end of the mature form, were confirmed
R:Webb, A.C.; DiPaello, C.A.; Rosenmasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au
Adv. Gene Technol. 22, 339-340, 1985
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A:Reference number: I51852
A:Accession: I51852
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Cross-references: GB:M54333; NID:G186287; PIDN:AAA59136.1; PID:G186288
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A:Reference number: A94023; PMID:85088517; PMID:6083565
A:Accession: A94023
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-269 <AUR>
A:Cross-references: GB:K02370; NID:G186268; PIDN:AAA6106.1; PID:G307043
R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gallie, S.
Nature 315, 641-647, 1995
A:Title: Cloning, sequence and expression of two distinct human interleukin-1 complement
A:Reference number: A93361; PMID:85240547; PMID:2389698
A:Accession: A93361
A:Molecule type: mRNA
A:Residues: 1-269 <MAR>
A:Cross-references: GB:K02532; NID:G33789; PIDN:CAA26372.1; PID:G33790
A:Note: parts of this sequence, including the amino end of the mature form, were confirmed
R:Webb, A.C.; DiPaello, C.A.; Rosenmasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au
Adv. Gene Technol. 22, 339-340, 1985
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A:Reference number: I51852
A:Accession: I51852
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Cross-references: GB:M54333; NID:G186287; PIDN:AAA59136.1; PID:G186288
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A:Reference number: A94023; PMID:85088517; PMID:6083565
A:Accession: A94023
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-269 <AUR>
A:Cross-references: GB:K02370; NID:G186268; PIDN:AAA6106.1; PID:G307043
R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gallie, S.
Nature 315, 641-647, 1995
A:Title: Cloning, sequence and expression of two distinct human interleukin-1 complement
A:Reference number: A93361; PMID:85240547; PMID:2389698
A:Accession: A93361
A:Molecule type: mRNA
A:Residues: 1-269 <MAR>
A:Cross-references: GB:K02532; NID:G33789; PIDN:CAA26372.1; PID:G33790
A:Note: parts of this sequence, including the amino end of the mature form, were confirmed
R:Webb, A.C.; DiPaello, C.A.; Rosenmasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au
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A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A:Reference number: I51852
A:Accession: I51852
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Cross-references: GB:M54333; NID:G186287; PIDN:AAA59136.1; PID:G186288
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A:Reference number: A94023; PMID:85088517; PMID:6083565
A:Accession: A94023
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-269 <AUR>
A:Cross-references: GB:K02370; NID:G186268; PIDN:AAA6106.1; PID:G307043
R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gallie, S.
Nature 315, 641-647, 1995
A:Title: Cloning, sequence and expression of two distinct human interleukin-1 complement
A:Reference number: A93361; PMID:85240547; PMID:2389698
A:Accession: A93361
A:Molecule type: mRNA
A:Residues: 1-269 <MAR>
A:Cross-references: GB:K02532; NID:G33789; PIDN:CAA26372.1; PID:G33790
A:Note: parts of this sequence, including the amino end of the mature form, were confirmed
R:Webb, A.C.; DiPaello, C.A.; Rosenmasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au
Adv. Gene Technol. 22, 339-340, 1985
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A:Reference number: I51852
A:Accession: I51852
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Cross-references: GB:M54333; NID:G186287; PIDN:AAA59136.1; PID:G186288
A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <MEB>
A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A:Reference number: A94023; PMID:85088517; PMID:6083565
A:Accession: A94023
A:Molecule type: mRNA
A:Residues: 1-5, 'K', 7-269 <AUR>
A:Cross-references: GB:K02370; NID:G186268; PIDN:AAA6106.1; PID:G307043
R:March, C.J.; Mosley, B.; Larsen, A.;

A>Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
A:Reference number: I52217; MUID:87156769; PMID:3493774
A:Accession: 165200
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-269 <NTS>
A:Cross-references: GB:M5330; NID:g166283; PIDN:AAA59135.1; PID:g37045
R:Kotenko, S.V.; Bulunov, M.T.; Velko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emelianov, I.I.; S.A.; Vinetkii, Y.P.
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
A>Title: Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin-1 beta.
A:Reference number: I38131; MUID:90249285; PMID:2635664
A:Accession: I38132
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-269 <KOT>
A:Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663
R:Zeebo, K.M.; Wuych, J.; Yuchenkoff, V.N.; Lu, H.; Hunt, P.; Duker, P.P.; Langley, K.
Blood 71, 962-968, 1988
A>Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic
A:Reference number: A90732; MUID:88184226; PMID:3281727
A:Accession: B27616
A:Molecule type: protein
A:Residues: 117-123, 'X', 125-126, 'X', 128 <ZSE>
R:Stevenson, F.T.; Bursien, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
A>Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysines
A:Reference number: A48293; MUID:93348250; PMID:8346241
A:Contents: annotation; myristylation of lysines
R:Nandori, V.B.; Hulse, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.
Biochim. Biophys. Acta 1118, 25-35, 1991
A>Title: The role of arginine residues in interleukin 1 receptor binding.
A:Reference number: S19608; MUID:92110334; PMID:1837236
A:Contents: annotation; type 1 IL-1 receptor interaction site
A>Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
R:Clare, G.M.; Gronenborn, A.M.
submitted to the Brookhaven Protein Data Bank, January 1991
A:Reference number: A50049; PDB:611B
A:Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
R:Clare, G.M.; Wingfield, P.T.; Gronenborn, A.M.
Biochemistry 30, 2315-2323, 1991
A>Title: High-resolution three-dimensional structure of interleukin beta in solution by
A:Reference number: A44675; MUID:91159409; PMID:2001363
A:Contents: annotation; (1)H-NMR structural determination
R:Harad, D.J.; Strickler, J.; Simon, P.; Young, P.R.
J. Biol. Chem. 266, 7081-7086, 1991
A>Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a conformational change.
A:Reference number: A39774; MUID:91201363; PMID:2016316
A:Contents: annotation
R:Finzel, B.C.; Watenpugh, K.D.; Einspahr, H.M.
submitted to the Brookhaven Protein Data Bank, December 1989
A:Reference number: A50016; PDB:111B
A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
R:Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpugh, K.D.; Einspahr, R.J.
Mol. Biol. 209, 779-791, 1989
A>Title: Crystal structure of recombinant human interleukin-beta at 2.0 angstrom resolution.
A:Reference number: A44666; MUID:90064532; PMID:2585509
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage of form of interleukin-beta, unlike interleukin 1-alpha, is inactive.
C:Comment: Interleukin-beta precursor is less heavily myristoylated than interleukin-1a
C:Genetics:
A:Gene: GDB:IL1B
A:Cross-references: GDB:120094; OMIM:147720
A:Map position: 2q13-q21
A:Introns: 16/2; 33/3; 101/1; 156/1; 199/3
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage
F:11-269/Product: interleukin-1 beta (status experimental <IL1>
F:76/Binding site: myristate (Lys) (covalent) (partial) (status experimental
F:123/Binding site: carbohydrate (Asn) (covalent) (status absent

Oy Best Local Similarity 28.0%; Pred. No.0.14; Matches 42; Conservative 27; Mismatches 65; Indels 16; Gaps 8;
 Db 28 NSALCRGKVKYNLPKKSIIHQDHKVLVLDSC--NLIAVPDKNY-IRPEIFALMSLS 84
 110 NEAVVADPAVPSLNL---CTLRDSQKSLVM-SGYELKHLHQQGDMEQGVFSMSVQG 165
 Oy SASAEKSGPILLVGSGEGFYLC--DKDQSGHPSILKKEKMLKLAQKESARRPFIY 142
 166 EESNDK-IPVALGLKEKRLYLSCVLKDKDCK----PTQL--EESVDPKNYPKKMKREKRVFN 218
 Db 143 RAQVGSNMNLESAAHPGWFICTSCNCEPV 172
 219 KIEINNKLEFESAGQFPNNWYISTSAENMPV 248
 RESULT 13
 B25528
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #ext_change 22-Jun-1999
 C:Accession: B25528
 R:Stevenson, B.J.; Hagenbueche, O.; Wellauer, P.K.
 Nucleic Acids Res. 14, 8307-8330, 1986
 A>Title: Sequence organisation and transcriptional regulation of the mouse elastase II ar
 A:Reference number: A93646; MUID:87066713; PMID:3641189
 A:Accession: B25528
 A:Molecule type: mRNA
 A:Residues: 1-246 <STS>
 C:Cross-references: GB:X04574; MID:954918; PID:CAA28243.1; PID:954919
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
 F:1-23/Domain: signal sequence #status: predicted <SIG>
 F:1-246/Product: trypsin #status: predicted <MAT>
 F:24-239/Domain: trypsin homology <TRY>
 F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status: predicted
 F:63,107,200/Active site: His, Asp, Ser #status: predicted
 F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status: predicted
 Query Match 9.0%; Score 95.5; DB 2; Length 246;
 Best Local Similarity 34.0%; Pred. No.0.21; Matches 36; Conservative 8; Mismatches 19; Indels 43; Gaps 5;
 Oy 1 MSALLILLVGAADVDDDDKLAANSAALCRGPVKVKNLPKFS-----IH 48
 1 MSALLILLVGAADVDPVDDDKIVGGYT--CRSSV---PYQSLNAGYHFCGSSLIN 54
 Db 49 DQ-----DHKVLVL-----DSGNLIAVPDKN 69
 55 DQWVSAHCKYKRIQVRLGHEHNINVLSENGEQVDSAKIIRHNNYN 100
 RESULT 14
 A30584
 A:Interleukin-1 beta precursor - rabbit
 N:Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating factor
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 25-May-1988 #sequence_revision 22-Nov-1996 #ext_change 22-Jun-1999
 C:Accession: A27714; A30584; J00082; A32166
 R:Morici, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
 Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
 A>Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiating factor
 A:Reference number: A27714; MUID:88134238; PMID:2449207
 A:Accession: A27714
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-268 <MOR>
 R:Cannon, U.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello, C.
 J. Immunol. 142, 2299-2306, 1989
 A>Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
 A:Reference number: A30584; MUID:89176242; PMID:2784458
 A:Accession: A30584
 A:Molecule type: mRNA

A:Residues: 1-268 <CAN>
A:Cross-references: GB:M26295; NID:G516632; P1DN:AA31373.1; PID:G516633
R:Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A:Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and
A:Reference number: A94230; MUID:89315718; PMID:2787507
A:Accession: J00082
A:Molecule type: mRNA
A:Residues: 1-268 <YOU>
A:Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1 beta, unlike interleukin-1 alpha, is inactive.
C:Comment: Interleukin-1 beta precursor is less heavily myristoylated than interleukin-1
C:Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F:117-268/Product: interleukin-1 beta #status predicted <IIB>

Query Match 8.7%; Score 92.5; DB 1; Length 268;
Best Local Similarity 24.7%; Pred. No. 0.44;
Matches 44; Conservative 26; Mismatches 81; Indels 27; Gaps 7;

QY 16 DYKDDDKLAANALCGPKVKNLPPKFSIHODHKVLYDSGNLIAVDPKN--YIRP 73
DB 110 DYSLECD---AVRSIHCR-----LQDAQKSLVLSGYELKALHNAENLNQ 153
QY 74 EIPFALASSLSASAEKSGSPILLGVSKGEFCLYC--DKDKGSHPSLQKKKXLMKLAQ 131
DB 154 QVFSMSVVGEBESNDK-IPVALGLRGKLYLSCVMKDK---PTLQL--ESVDPNRY 206

QY 132 KESARPFIFYRAQVGSNNMLESAHPGMFICTSCNCPNCPVGVTDKFNRRKHIEFSFQ 189
DB 207 KKKMEKRVFVKIEIKDLFEFSAQFPWYISTSGTEYMPVFLGNSGQDLIDPSME 264

RESULT 15
S34031
KTR3 protein - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YBR145; protein YBR205W
C:Species: Saccharomyces cerevisiae
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: S34031; S46077; S34928
R:Jacquet, M.
Submitted to the EMBL Data Library, January 1993
A:Reference number: S34022
A:Accession: S34031
A:Molecule type: DNA
A:Residues: 1-404 <JAC>
A:Cross-references: EMBL:Z21487; NID:G311665; PID:G311682
R:Busseau, F.; Demolis, N.; Jacquet, M.; Maillet, L.
Submitted to the Protein Sequence Database, August 1994
A:Reference number: S46054
A:Accession: S46077
A:Molecule type: DNA
A:Residues: 1-404 <BUS>
A:Cross-references: EMBL:Z36074; NID:G536582; PID:G536583; MIPS:YBR205W
R:Busseau, F.; Maillet, L.; Gallion, L.; Jacquet, M.
Yeast 9, 797-806, 1993
A:Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome II
A:Reference number: S34925; MUID:93377417; PMID:8368014
A:Accession: S34928
A:Molecule type: DNA
A:Residues: 91-352 <BU2>
A:Cross-references: EMBL:Z21487
C:Gene: SCD:KTR3
A:Cross-references: SGD:S0000409; MIPS:YBR205W
A:Map position: 2R
C:Keywords: transmembrane protein
F:22-45/Domain: transmembrane #status predicted <TM>

Query Match 8.6%; Score 91; DB 2; Length 404;
Best Local Similarity 22.8%; Pred. No. 0.99;
Matches 36; Conservative 20; Mismatches 58; Indels 44; Gaps 5;

QY 46 SIHQDHRVLYDSGNLIAVDPKNYIRPE-----IPFALASSLSASAEKSGSPIL 95
DB 2 SVH---HKKLMPSALIRYQGISSFFGLIIVLSFLFFMGSRSPVPIAQTIVS 58
QY 96 LGVSKGEFCLYCDKQSGSHPSLQKKKXLMKLAOKESARPFIFYRAQVGSNNMLESA 155
DB 59 RVASKDYLMPPTDSQGVIRHVDGKKKKGVMTIARNS-----DLNVLVXSI 106

QY 156 AHPGMFICTSCNCPNCPVGVTDKFNRRKHIEFSF---QP 190
DB 107 RH-----VEDRFNNRYHYDVPFLNDQP 128

Search completed: September 9, 2004, 13:28:28
Job time : 42 secs

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